

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 03:53:44 ; Search time 3506.39 Seconds  
(without alignments)  
3255.375 Million cell updates/sec

Title: US-10-635-908-6  
Perfect score: 617  
Sequence: 1 DVXLVBSGGGLVKGSLKLT.....RSGYFMDYGOCTSVTVS 119

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues  
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ .p2n.model -DEV=rlh  
-Q=/abs/ABSSWEB.spool/US10635908/runat\_02062006\_104214\_10235/app\_query.fasta\_1  
-DB=GenEmbl -OPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPLC=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=pcp -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTPRM=pcp -NORW=exr -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h  
-USRR=US10635908 @CCN\_1\_15767 @runat\_02062006\_104214\_10235 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_srs:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_hlg:\*  
13: gb\_in:\*  
14: gb\_cm:\*  
15: gb\_da:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	617	100.0	357	2 AX556872 Sequence
2	617	100.0	1056	2 AX363232 Sequence
3	617	100.0	1411	2 AX363234 Sequence

4	617	100.0	1702	2 AX363235	AX363235 Sequence
5	617	100.0	2431	2 AX614787	AX614787 Sequence
6	559	90.6	432	6 MMIGHV3B6	X91667 M.musculus
7	559	90.6	432	6 MMIGHV5A6	X91668 M.musculus
8	559	90.6	474	2 AR080862	AR080862 Sequence
9	559	90.6	474	2 AR080864	AR080864 Sequence
10	539	87.4	422	2 BD260215	BD260215 Somatic t
11	539	87.4	422	2 BD260216	BD260216 Somatic t
12	539	87.4	422	2 AX042383	AX042383 Sequence
13	539	87.4	422	2 AX042384	AX042384 Sequence
14	537.5	87.1	419	2 BD260217	BD260217 Somatic t
15	537.5	87.1	419	2 BD260218	BD260218 Somatic t
16	533.5	86.5	419	2 AX042386	AX042386 Sequence
17	533.5	86.5	419	2 AF052835	AF052835 Mus muscu
18	530.5	86.0	1671	6 AF052835	AF052835 Mus muscu
19	529.5	85.8	360	6 MUSIGH2PRA	M26986 Mus muscu
20	516.5	83.7	339	6 MMIGHV62	Y00744 Mouse rear
21	514.5	83.4	342	6 MMIGHV62	X65785 M.musculus
22	513	83.1	735	2 E13598	E13598 DNA encodin
23	512.5	83.1	360	6 MUSIGH3C2A	L30142 Mus muscu
24	511.5	82.9	360	6 AY674872	AY674872 Mus muscu
25	511.5	82.9	360	6 AY674873	AY674873 Mus muscu
26	511.5	82.9	360	6 MUSIGH3E5A	L31896 Mus muscu
27	511	82.8	363	2 E12951	E12951 DNA encodi
28	511	82.8	363	2 E13910	E13910 DNA encodin
29	510.5	82.7	501	6 MUSIGHV	L41626 Mus muscu
30	506	82.0	363	2 E13912	E13912 DNA encodin
31	505.5	81.9	360	6 MUS2H1VH	L05431 Mouse mRNA
32	502	81.4	354	2 E16083	E16083 cDNA encodi
33	500.5	81.1	366	2 BD174582	BD174582 Gene enco
34	500.5	81.1	366	6 AB079937	AB079937 Mus muscu
35	500.5	81.1	1671	6 AF052834	AF052834 Mus muscu
36	499	80.9	339	6 MUSIGC	I23152 Mus muscu
37	498	80.7	484	2 AR648819	AR648819 Sequence
38	497.5	80.6	360	6 MMU309276	AJ309276 Mus muscu
39	495.5	80.3	364	6 MDIGMVB	Z22122 M.domesticu
40	494.5	80.1	669	6 MMU62650	U62650 Mus muscu
41	494	80.1	363	6 AF178589	AF178589 Mus muscu
42	493	79.9	354	6 MMVHMR2	X63798 M.musculus
43	492.5	79.8	378	6 AY648638	AY648638 Mus muscu
44	491	79.6	369	6 MMU277218	AJ277218 Mus muscu
45	490	79.4	369	6 MMU277220	AJ277220 Mus muscu

## ALIGNMENTS

RESULT 1  
AX556872  
LOCUS AX556872 357 bp DNA  
DEFINITION Sequence 1 from Patent WO02062972.  
ACCESSION AX556872  
VERSION AX556872.1 GI:25899970  
SOURCE  
ORGANISM  
synthetic construct  
other sequences: artificial sequences.  
REFERENCE  
AUTHORS Oosterwijk,E., Warnaar,S. and Ullrich,S.  
TITLE Hybridoma cell line g250 and its use for producing monoclonal  
antibodies  
JOURNAL Patent: WO 02062972-A 1 15-AUG-2002;  
Wiley AG (DE)  
location/Qualifiers  
source 1..357  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="mouse/human chimeric antibody gene"

ORIGIN  
Alignment Scores:  
Pred. No.: 3,896-67 Length: 357  
Score: 617.00 Matches: 119



[illegible]

	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="primer"		
ORIGIN			
Alignment Scores:			
Pred. NO.:	2.81e-66	Length:	2431
Score:	617.00	Matches:	119
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0
US-10-635-908-6 (1-119) x AX614787 (1-2431)			
Oy	1 AspvallysleuValIGuserglYglYglYleuVallylsleuglYglYserLeuLyseu 20 		
Dd	843 GACGGTAAGCTCGGGAAGTCTGGGGAGAGCCTTAGTAAGCTTGAGAGGTCCCTAAATC 902 		
Oy	21 SerCyalaalaserGlYphetrPhesernanTYrMetSerTrpValargInthr 40 		
Dd	903 TCCTGTGAGCCTCGAGTCACTTCCTAGTAATAAACAAGTCCTGGGTTGCAGACT 962 		
Oy	41 ProglulysatgleuGluLeuValAlAlalehsenarSpGlYglYlleThrTYr 60 		
Dd	963 CCAGAGAAGAGCGTGAAGTTGTGGCACACCATTAAATGATGGGGATACCACTACAT 1022 		
Oy	61 LeuapThrVallysglYArghPheThrIleserArgaPaanaAlalyAsnThrLeuTYr 80 		
Dd	1023 CTAGACACTGMAAGGCCCATTCACCATTCMAAGAGCANATGCCAAGAACACCCCTGAC 1082 		
Oy	81 LeuginMetSerSerleuLYseSerGluaspThrAlaleuPheTYrCyalaargHilarg 100 		
Dd	1083 CTGCAATAGACACAGCTGAAGTCTGAGACACAGCGCTTGTTACTGTGCAAGACACCGC 1142 		
Oy	101 SerGIYrPheserMetAspTYrTrglYgIngIYrThrservalThVaISerSer 119 		
Dd	1143 TCGGCTCACTTCTATAGACTACTGGGGCTCAAGAACCTCAGTACCCGTCTCTCA 1199 		
RESULT 6			
NMIGHV3B6			
LOCUS		432 bp	mRNA linear ROD 24-OCT-1995
DEFINITION	M.musculus mRNA for Ig heavy chain variable region (cell line 3B6)		
ACCESSION	X91867		
VERSION	X91867.1 GI:100180		
KEYWORDS	complementarity determining region; heavy chain; immunoglobulin variable region.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.		
AUTHORS	Carceller,A., Rosell-Vives,E., Gomez-Rois,A., Adan,J., Sproll,M. and Puigals,J.		
TITLE	Immunological and structural properties of anti-idiotypic antibodies mimicking an epitope of human epidermal growth factor receptor		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 432)		
AUTHORS	Rosell-Vives,E.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-SEP-1995) E. Rosell-Vives, MERCK, Farma y Quimica S.A., Caspe 108, E-08010 Barcelona, SPAIN		
FEATURES	Location/Qualifiers		
source	1..432		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/strain="BALB/c"		
	/sub_strain="by J Ico"		
	/db_xref="taxon:10090"		
	/chromosome="12"		

```

CDS
/cell_line="3B6"
/cell_type="fusion of splenocytes x H1i friendly myeloma
653"
/issue_type="hybridoma"
1..>432
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="CAA62854.1"
/db_xref="GI:1008125"
/translation="MDSRLNLFVLVLRKVLCDVLRVSGGGLVKGSLKLSCAAS
GFTFSNYMSWRQTPKRLFEVAALNSGSGTTPDYKGFTRSRDANKTVLYQM
SLKSEDTALYCARHRRDSSGYGVALDWGGTSVVS"
1..57
sig_peptide
1..432
/product="variable region of Ig heavy chain"
148..162
/misc_feature
/feature="CDR1"
/note="complementarity-determining region 1"
205..255
/product="CDR2"
/note="complementarity-determining region 2"
352..399
/product="CDR3"
/note="complementarity-determining region 3"

misc_feature
misc_feature
misc_feature

ORIGIN
Alignment Scores:
Pred. No.: 7.65e-60 Length: 432
Score: 559.00 Matches: 111
Percent Similarity: 92.8% Conservative: 5
Best Local Similarity: 88.8% Mismatches: 3
Query Match: 90.6% Indels: 6
DB: Gaps: 2

US-10-635-908-6 (1-119) x MMIGHV3B6 (1-432)
QY 1 AapVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuVal 20
Db 58 GAGGTGAAGCTCTGGAGTCTGGGGAGGCTTGTGAAGCTTGGAGGCTCCGGAAC 117
QY 21 SerCyAlAlAlSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
Db 118 TCCTGTGACGCGCTCGATTCACTTCAGTAATTAATTAATGCTGGGTGCCAGACT 177
QY 41 ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
Db 178 CCAGAGAAAGAGGTGGAGTTTGGCAGCCATTAAATGTAATGTGTGTGACACTTAT 237
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTyr 80
Db 238 CCAGACACTGTGAAGGCGGATTCACCACTCCAGAGCAATGCCAAGAACACCTGTAC 297
QY 81 LeuGlnMetSerSerLeuValSerGlyAspThrAlaIleuPheTyrCyAlAlaArgHisArg 100
Db 298 CTGCATATGAGCAGTCTGAAGTCTGAGACACAGCCTTGATTAATCTGTGCAAGACATCG 357
QY 101 -----SerGlyTyr-----PheSerMetAspTyrTyrGlyGlnGlyThrSer 114
Db 358 GGGAGAGACAGCTCCGGGCTTACCTAGAGGTATGCTATGACTACTAGGGGTCAAGGAACCTCA 417
QY 115 ValThrValSerSer 119
Db 418 GTCAACCTCTCTCA 432

RESULT 7
LOCUS MMIGHV5A6 432 bp mRNA linear ROD 24-OCT-1995
DEFINITION M.musculus mRNA for Ig heavy chain variable region (cell line 5A6).
ACCESSION X91668
VERSION X91668.1 GI:1001881
KEYWORDS complementarity determining region; heavy chain; immunoglobulin
variable region.
SOURCE Mus musculus (house mouse)

```

```

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1
Carceller, A., Rosell-Vives, E., Gomez-Rold, A., Adan, J., Sproll, M.
and Puigade, J.
TITLE
Immunological and structural properties of anti-idiotypic
antibodies mimicking an epitope of human epidermal growth factor
receptor
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 432)
AUTHORS
Rosell-Vives, E.
TITLE
Direct Submission
JOURNAL
Submitted (19-SEP-1995) E. Rosell-Vives, MERCK, Farma y Quimica
S.A., Caspe 108, E-08010 Barcelona, SPAIN

FEATURES
source
1..432
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/sub_strain="by J Ico"
/db_xref="taxon:10090"
/chromosome="12"
/cell_line="5A6"
/cell_type="fusion of splenocytes x H1i friendly myeloma
653"
/issue_type="hybridoma"
1..>432
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="CAA62855.1"
/db_xref="GI:1008126"
/translation="MDFGLSLFLVLRKVLCDVLRVSGGGLVKGSLKLSCAAS
GFTFSNYMSWRQTPKRLFEVAALNSGSGTTPDYKGFTRSRDANKTVLYQM
SLKSEDTALYCARHRRDSSGYGVALDWGGTSVVS"
1..57
sig_peptide
1..432
/product="variable region of Ig heavy chain"
148..162
/misc_feature
/feature="CDR1"
/note="complementarity-determining region 1"
205..255
/product="CDR2"
/note="complementarity-determining region 2"
352..399
/product="CDR3"
/note="complementarity-determining region 3"

ORIGIN
Alignment Scores:
Pred. No.: 7.65e-60 Length: 432
Score: 559.00 Matches: 111
Percent Similarity: 92.8% Conservative: 5
Best Local Similarity: 88.8% Mismatches: 3
Query Match: 90.6% Indels: 6
DB: Gaps: 2

US-10-635-908-6 (1-119) x MMIGHV5A6 (1-432)
QY 1 AapVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuVal 20
Db 58 GAGGTGAAGCTCTGGAGTCTGGGGAGGCTTGTGAAGCTTGGAGGCTCCGGAAC 117
QY 21 SerCyAlAlAlSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
Db 118 TCCTGTGACGCGCTCGATTCACTTCAGTAATTAATTAATGCTGGGTGCCAGACT 177
QY 41 ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
Db 178 CCAGAGAAAGAGGTGGAGTTTGGCAGCCATTAAATGTAATGTGTGTGACACTTAT 237
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTyr 80

```



Db 238 CCAGACACTGTGAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 297  
Qy 81 LeuGImetSerSerleuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100  
Db 298 CTGCAGAAATGAGCAGTCTGAGAGTCTGAGACACAGCCCTTGATTAATCTGTGCAAGACATCG 357  
Qy 101 -----SerGlyTyr-----PheSerMetAspTyrTrpGlyGlnGlyThrSer 114  
Db 358 GGGAGGAGCAGCTCGGGCTACGATGAGGTATGATAGACTACTGGGGTCAAGAACTCA 417  
Qy 115 ValThrValSerSer 119  
Db 418 GTCACCGCTCTCTCA 432  
RESULT 8  
AR080862  
LOCUS AR080862 474 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 5 from patent US 5969107.  
ACCESSION AR080862  
VERSION AR080862.1 GI:10007591  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 474)  
TITLE Carcellier,A., Rosell,E., Gomez,A., Adan,J. and Piuats,J.  
Anti-idiotypic antibodies which induce an immune response against  
epidermal growth factor receptor  
JOURNAL Patent: US 5969107-A 5 19-OCT-1999;  
FEATURES  
source 1..474  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 8,42e-60 Length: 474  
Score: 559.00 Matches: 111  
Percent Similarity: 92.8% Conservative: 5  
Best Local Similarity: 88.8% Mismatches: 3  
Query Match: 90.6% Indels: 6  
Gaps: 2  
DB: 2  
US-10-635-908-6 (1-119) x AR080862 (1-474)  
Qy 1 AspValLysLeuValGluSerGlyGlyLeuValLysLeuGlySerLeuLysLeu 20  
Db 58 GACGTGAAGCTCGTGGAGCTGGGGGAGGCTTAGTGAAGCTGGAGGCTCCCGAAACTA 117  
Qy 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgInThr 40  
Db 118 TCCTGTGACACCTCTGATTCACCTTCAGTAATTAATGATGATGTTGGTCCCAACT 177  
Qy 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyr 60  
Db 178 CCAGAGAAAGGCGCTGAGTCTGAGACACAGCCCTTGATTAATCTGTGCAAGACATCG 237  
Qy 61 LeuAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80  
Db 238 CCAGACACTGTGAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 297  
Qy 81 LeuGImetSerSerleuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100  
Db 298 CTGCAGAAATGAGCAGTCTGAGAGTCTGAGACACAGCCCTTGATTAATCTGTGCAAGACATCG 357  
Qy 101 -----SerGlyTyr-----PheSerMetAspTyrTrpGlyGlnGlyThrSer 114  
Db 358 GGGAGGAGCAGCTCGGGCTACGATGAGGTATGATAGACTACTGGGGTCAAGAACTCA 417  
Qy 115 ValThrValSerSer 119  
Db 418 GTCACCGCTCTCTCA 432

RESULT 9  
AR080864  
LOCUS AR080864 474 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 9 from patent US 5969107.  
ACCESSION AR080864  
VERSION AR080864.1 GI:10007593  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 474)  
TITLE Carcellier,A., Rosell,E., Gomez,A., Adan,J. and Piuats,J.  
Anti-idiotypic antibodies which induce an immune response against  
epidermal growth factor receptor  
JOURNAL Patent: US 5969107-A 9 19-OCT-1999;  
FEATURES  
source 1..474  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 8,42e-60 Length: 474  
Score: 559.00 Matches: 111  
Percent Similarity: 92.8% Conservative: 5  
Best Local Similarity: 88.8% Mismatches: 3  
Query Match: 90.6% Indels: 6  
Gaps: 2  
DB: 2  
US-10-635-908-6 (1-119) x AR080864 (1-474)  
Qy 1 AspValLysLeuValGluSerGlyGlyLeuValLysLeuGlySerLeuLysLeu 20  
Db 58 GACGTGAAGCTCGTGGAGCTGGGGGAGGCTTAGTGAAGCTGGAGGCTCCCGAAACTC 117  
Qy 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgInThr 40  
Db 118 TCCTGTGACACCTCTGATTCACCTTCAGTAATTAATGATGATGTTGGTCCCAACT 177  
Qy 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyr 60  
Db 178 CCAGAGAAAGGCGCTGAGTCTGAGACACAGCCCTTGATTAATCTGTGCAAGACATCG 237  
Qy 61 LeuAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80  
Db 238 CCAGACACTGTGAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 297  
Qy 81 LeuGImetSerSerleuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100  
Db 298 CTGCAGAAATGAGCAGTCTGAGAGTCTGAGACACAGCCCTTGATTAATCTGTGCAAGACATCG 357  
Qy 101 -----SerGlyTyr-----PheSerMetAspTyrTrpGlyGlnGlyThrSer 114  
Db 358 GGGAGGAGCAGCTCGGGCTACGATGAGGTATGATAGACTACTGGGGTCAAGAACTCA 417  
Qy 115 ValThrValSerSer 119  
Db 418 GTCACCGCTCTCTCA 432  
RESULT 10  
BD260215  
LOCUS BD260215 422 bp DNA linear PAT 17-JUL-2003  
DEFINITION Somatic transgene immunization and related methods.  
ACCESSION BD260215  
VERSION BD260215.1 GI:33069985  
KEYWORDS UP 2002542305-A/4.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 422)  
AUTHORS Zanetti,M.  
TITLE Somatic transgene immunization and related methods

JOURNAL Patent: JP 2002542305-A 4 10-DEC-2002;  
MAURIZIO ZANETTI, EUROGEN HOLDING SA  
COMMENT OS Artificial Sequence  
PN JP 2002542305-A/4  
PD 10-DEC-2002  
PF 27-APR-2000 JP 2000613478  
PR 27-APR-1999 US 09/300959  
PI MAURIZIO ZANETTI  
PC A61K48/00, A61K31/711, A61K35/76, A61K38/00, A61K38/22, A61K38/36,  
A61K39/395,  
A61K37/46,  
PC A61P31/12, A61P37/04, C12N5/10, C12N15/09, A61K37/02, A61K37/24, PC  
A61K37/46,  
PC C12N15/00, C12N5/00  
CC Description of Artificial Sequence: genomic VDJ region FH  
Key Location/Qualifiers  
FT source 1..422  
FT Location/Qualifiers  
FT /organism='Artificial Sequence'.  
FEATURES  
source 1..422  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Alignment Scores:  
Pred. No.: 2,29e-57 Length: 422  
Score: 539.00 Matches: 107  
Percent Similarity: 91.6% Conservative: 2  
Best Local Similarity: 89.9% Mismatches: 10  
Query Match: 87.4% Indels: 0  
DB: 2 Gaps: 0

US-10-635-908-6 (1-119) x BD260215 (1-422)

QY 1 AapvallyleuValylGusergylYglYleuVallyleuGlyYserleuylsleu 20  
DB 1 GACGTAAAGCTGTGAGTCTGGGGAGGCTTAGTAAGCTTGAGAGGTCCTGAAACCTC 60  
QY 21 SerCyAlAlaSerGlyPheThrPheSerAenTYrTYrMetSerTrpValArgGlnThr 40  
DB 61 TCTGTGACGCTCTGGATTCACTTCAGTAGGTAATTACATGCTTGCGGTTGCCAGACT 120  
QY 41 ProGluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyYlleThrTYrTYr 60  
DB 121 CCAAGAAAGAGCTGGAAGTTGGTCGAGCATTTAAATGTAATGTTGTGACACTACTAT 180  
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTYr 80  
DB 181 CCAGACACTGTGAAGGCGGATTCACCACTCTCCAGAGCAATGCCAAAAACACCTGTAC 240  
QY 81 LeuGlnMetSerSerleuYsSerGluAspThrAlaLeuPheTYrCYsAlaArgHisArg 100  
DB 241 CTGCAATAGAGAGCTGGAAGTCTGAGACACAGCCCTTGATTACTGTCCAAAGAAAGTA 300  
QY 101 SerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThrValSerSer 119  
DB 301 CCTACTCTCATGATGATGACTACTGGGTCAGAGAAACCTCAAGTCAACGCTCTCTCA 357

RESULT 11  
BD260216 422 bp DNA linear PAT 17-JUL-2003  
LOCUS BD260216  
DEFINITION Somatic transgene immunization and related methods.  
ACCESSION BD260216  
VERSION BD260216.1 GI:33069986  
KEYWORDS JP 2002542305-A/5.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 422)  
AUTHORS Zanetti, M.  
TITLES Somatic transgene immunization and related methods  
JOURNAL Patent: JP 2002542305-A 5 10-DEC-2002;  
MAURIZIO ZANETTI, EUROGEN HOLDING SA

COMMENT OS Artificial Sequence  
PN JP 2002542305-A/5  
PD 10-DEC-2002  
PF 27-APR-2000 JP 2000613478  
PR 27-APR-1999 US 09/300959  
PI MAURIZIO ZANETTI  
PC A61K48/00, A61K31/711, A61K35/76, A61K38/00, A61K38/22, A61K38/36,  
A61K39/395,  
A61K37/46,  
PC A61P31/12, A61P37/04, C12N5/10, C12N15/09, A61K37/02, A61K37/24, PC  
A61K37/46,  
PC C12N15/00, C12N5/00  
CC Description of Artificial Sequence: genomic VDJ region FH  
Key Location/Qualifiers  
FT source 1..422  
FT Location/Qualifiers  
FT /organism='Artificial Sequence'.  
FEATURES  
source 1..422  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Alignment Scores:  
Pred. No.: 2,29e-57 Length: 422  
Score: 539.00 Matches: 107  
Percent Similarity: 91.6% Conservative: 2  
Best Local Similarity: 89.9% Mismatches: 10  
Query Match: 87.4% Indels: 0  
DB: 2 Gaps: 0

US-10-635-908-6 (1-119) x BD260216 (1-422)

QY 1 AapvallyleuValylGusergylYglYleuVallyleuGlyYserleuylsleu 20  
DB 1 GACGTAAAGCTGTGAGTCTGGGGAGGCTTAGTAAGCTTGAGAGGTCCTGAAACCTC 60  
QY 21 SerCyAlAlaSerGlyPheThrPheSerAenTYrTYrMetSerTrpValArgGlnThr 40  
DB 61 TCTGTGACGCTCTGGATTCACTTCAGTAGGTAATTACATGCTTGCGGTTGCCAGACT 120  
QY 41 ProGluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyYlleThrTYrTYr 60  
DB 121 CCAAGAAAGAGCTGGAAGTTGGTCGAGCATTTAAATGTAATGTTGTGACACTACTAT 180  
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTYr 80  
DB 181 CCAGACACTGTGAAGGCGGATTCACCACTCTCCAGAGCAATGCCAAAAACACCTGTAC 240  
QY 81 LeuGlnMetSerSerleuYsSerGluAspThrAlaLeuPheTYrCYsAlaArgHisArg 100  
DB 241 CTGCAATAGAGAGCTGGAAGTCTGAGACACAGCCCTTGATTACTGTCCAAAGAAAGTA 300  
QY 101 SerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThrValSerSer 119  
DB 301 CCTACTCTCATGATGATGACTACTGGGTCAGAGAAACCTCAAGTCAACGCTCTCTCA 357

RESULT 12  
AX042383 422 bp DNA linear PAT 23-NOV-2000  
LOCUS AX042383  
DEFINITION Sequence 5 from Patent WO0064488.  
ACCESSION AX042383  
VERSION AX042383.1 GI:11341000  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Zanetti, M.  
TITLES Somatic transgene immunization and related methods  
JOURNAL Patent: WO 0064488-A 5 02-NOV-2000;  
Zanetti, Maurizio (US)  
FEATURES  
source 1..422  
Location/Qualifiers

ORIGIN

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="genomic VDJ region"

## Alignment Scores:

Pred. No.: 2,29e-57 Length: 422  
Score: 539.00 Matches: 107  
Percent Similarity: 91.6% Conservative: 2  
Best Local Similarity: 89.9% Mismatches: 10  
Query Match: 87.4% Indels: 0  
DB: 2 Gaps: 0

US-10-635-908-6 (1-119) x AX042383 (1-422)

QY 1 AspValLysLeuValGluSerGlyGlyLeuValLysLeuGlyGlySerLeuLysLeu 20  
DB 1 GACGTGAAGCTGTGAGTCTGGGGAGGCTTAGGAACTGGAGGGTCCCGAAATC 60  
QY 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40  
DB 61 TCTGTGCAGCCTCTGGATTCACTTTCAGTAGTATTACATGCTTGGGTTCCCGAGACT 120  
QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60  
DB 121 CCAGAGAAGAGCGTGGAGTTGTCGACGCCATTATATAGTAATGGTGTAGCACCCTACT 180  
QY 61 LeuAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80  
DB 181 CCAGACACTGTGAAGGCCGATTCCACCATCTCCAGAGACAAATGCCAAAAACACCTGTAC 240  
QY 81 LeuGluMetSerSerLeuLysSerGlyAspThrAlaLeuPheTyrCysAlaArgHisArg 100  
DB 241 CTGCAATATGACGCTGAAAGTCTGAGACACAGCCTTGATTACTGTGCAAGAAAGTA 300  
QY 101 SerGlyTyrPheSerMetAspTyrTyrTrpGlyGlnGlyThrSerValThrValSerSer 119  
DB 301 CCTACTCTCATGTATGACTACTGCGGTCAAGAAACCTCAAGTCAACCGTCTCTCA 357

RESULT 13  
AX042384 422 bp DNA linear PAT 23-NOV-2000  
LOCUS  
DEFINITION Sequence 6 from Patent WO0064488.  
ACCESSION AX042384  
VERSION AX042384.1 GI:11341001

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1  
Zanetti, M.  
Somatic transgene immunization and related methods  
Patent: WO 0064488-A 6 02-NOV-2000;  
Zanetti, Maurizio (US)

FEATURES  
source  
1..422  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="genomic VDJ region"

## ORIGIN

Alignment Scores:  
Pred. No.: 2,29e-57 Length: 422  
Score: 539.00 Matches: 107  
Percent Similarity: 91.6% Conservative: 2  
Best Local Similarity: 89.9% Mismatches: 10  
Query Match: 87.4% Indels: 0  
DB: 2 Gaps: 0

US-10-635-908-6 (1-119) x AX042384 (1-422)

QY 1 AspValLysLeuValGluSerGlyGlyLeuValLysLeuGlyGlySerLeuLysLeu 20  
DB 1 GACGTGAAGCTGTGAGTCTGGGGAGGCTTAGGAACTGGAGGGTCCCGAAATC 60  
QY 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40  
DB 61 TCTGTGCAGCCTCTGGATTCACTTTCAGTAGTATTACATGCTTGGGTTCCCGAGACT 120  
QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60  
DB 121 CCAGAGAAGAGCGTGGAGTTGTCGACGCCATTATATAGTAATGGTGTAGCACCCTACT 180  
QY 61 LeuAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80  
DB 181 CCAGACACTGTGAAGGCCGATTCCACCATCTCCAGAGACAAATGCCAAAAACACCTGTAC 240  
QY 81 LeuGluMetSerSerLeuLysSerGlyAspThrAlaLeuPheTyrCysAlaArgHisArg 100  
DB 241 CTGCAATATGACGCTGAAAGTCTGAGACACAGCCTTGATTACTGTGCAAGAAAGTA 300  
QY 101 SerGlyTyrPheSerMetAspTyrTyrTrpGlyGlnGlyThrSerValThrValSerSer 119  
DB 301 CCTACTCTCATGTATGACTACTGCGGTCAAGAAACCTCAAGTCAACCGTCTCTCA 357

RESULT 14  
BD260217 419 bp DNA linear PAT 17-JUL-2003  
LOCUS  
DEFINITION Somatic transgene immunization and related methods.  
ACCESSION BD260217  
VERSION BD260217.1 GI:33069987  
KEYWORDS  
JP 2002542305-A/6.  
SOURCE  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 (bases 1 to 419)  
AUTHORS  
Zanetti, M.  
TITLE  
Somatic transgene immunization and related methods  
JOURNAL  
Patent: JP 2002542305-A 6 10-DEC-2002;  
MAURIZIO ZANETTI, EUROGEN HOLDING SA  
COMMENT  
OS Artificial Sequence  
PN JP 2002542305-A/6  
PD 10-DEC-2002 JP 200613478  
EP 27-APR-2000 JP 200613478  
PR 27-APR-1999 US 09/300959  
PI MAURIZIO ZANETTI  
PC A61K48/00, A61K31/711, A61K35/76, A61K38/00, A61K38/22, A61K38/36,  
PC A61K39/395,  
PC A61P31/12, A61P37/04, C12N5/10, C12N5/09, A61K37/02, A61K37/24, PC  
A61K37/46,  
PC C12N15/00, C12N5/00  
CC Description of Artificial Sequence: genomic VDJ region FH  
Key Location/Qualifiers  
FT source 1..419  
/organism="Artificial Sequence".

## FEATURES

source  
1..419  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

## ORIGIN

Alignment Scores:  
Pred. No.: 3,49e-57 Length: 419  
Score: 537.50 Matches: 107  
Percent Similarity: 92.4% Conservative: 3  
Best Local Similarity: 89.9% Mismatches: 8  
Query Match: 87.1% Indels: 1  
DB: 2 Gaps: 1

US-10-635-908-6 (1-119) x BD260217 (1-419)

QY 1 AspValLysLeuValGluSerGlyGlyLeuValLysLeuGlyGlySerLeuLysLeu 20  
DB 1 GACGTGAAGCTGTGAGTCTGGGGAGGCTTAGGAACTGGAGGGTCCCGAAATC 60

```

Db      1  GACGTGAAGCTGTGGAGCTTGGGGAGGCTTAGTGAAGCTTGGAGGGTCCCTGAAACTC 60
QY      21  SerCysAlaIaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40
Db      61  TCCTGTGACGCTCTGGATTCACTTTCAGTAGTATTACATGTCCTGGGTTGCCAGACT 120
QY      41  ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
Db      121  CCAGAGAAGAGGCTGGAGTTGGTCGACGATTAATAGTAAGTGTAGACCTACATAT 180
QY      61  LeuAspThrValIleGlyValArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTyr 80
Db      181  CCAGACACTGTGAAGGGCCGATTCCACCATCTCCAGACAAATGCCAAAACACCTGTAC 240
QY      241  CTGCAAAATGAGCAGTCTGAAGTCTGAGACACAGCCTGTATTACTGTGCAAGAAAGGCC 300
QY      101  SerGlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 119
Db      301  TACTCTCAT---GGTATGGACTACTGGGGTCAAGAACTCAGTCACCGTCTCTCA 354

```

## RESULT 15

```

AX042385      419 bp      DNA      linear      PAT 23-NOV-2000
LOCUS      AX042385      Sequence 7 from Patent WO0064488.
DEFINITION      AX042385
ACCESSION      AX042385
VERSION      AX042385.1  GI:11341002
KEYWORDS
SOURCE
ORGANISM      synthetic construct
              other sequences; artificial sequences.

```

```

REFERENCE
AUTHORS      Zanetti, M.
TITLE      Somatic transgene immunization and related methods
JOURNAL      Patent: WO 0064488-A 7 02-NOV-2000;
              Zanetti, Maurizio (US)
              location/Qualifiers

```

```

FEATURES
source
1..419
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="genomic VDJ region"

```

## ORIGIN

## Alignment Scores:

```

Pred. No.:      3,49e-57      Length:      419
Score:          537.50      Matches:      107
Percent Similarity: 92.4%      Conservative: 3
Best Local Similarity: 89.9%      Mismatches: 8
Query Match:    87.1%      Indels:      1
DB:              Gaps:      1

```

US-10-635-908-6 (1-119) x AX042385 (1-419)

```

QY      1  AapValIleValLeuValGluSerGlyGlyGlyLeuValIleGluGlyGlySerLeuIleVal 20
Db      1  GACGTGAAGCTGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGGAGGGTCCCTGAAACTC 60
QY      21  SerCysAlaIaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40
Db      61  TCCTGTGACGCTCTGGATTCACTTTCAGTAGTATTACATGTCCTGGGTTGCCAGACT 120
QY      41  ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
Db      121  CCAGAGAAGAGGCTGGAGTTGGTCGACGATTAATAGTAAGTGTAGACCTACATAT 180
QY      61  LeuAspThrValIleGlyValArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTyr 80
Db      181  CCAGACACTGTGAAGGGCCGATTCCACCATCTCCAGACAAATGCCAAAACACCTGTAC 240
QY      81  LeuGluMetSerSerLeuIleSerGlyAspThrAlaLeuPheTyrCysAlaArgHisArg 100

```

```

Db      241  CTGCAAAATGAGCAGTCTGAAGTCTGAGACACAGCCTGTATTACTGTGCAAGAAAGGCC 300

```

```

QY      101  SerGlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 119
Db      301  TACTCTCAT---GGTATGGACTACTGGGGTCAAGAACTCAGTCACCGTCTCTCA 354

```

Search completed: June 3, 2006, 06:56:33  
Job time : 3509.39 secs



```

XX 07-FEB-2001; 2001US-0266853P.
PR 05-OCT-2001; 2001US-0327008P.
XX (WILE-) WILEX AG.
XX Oosterwijk E, Wijnnaar S, Ulrich S;
XX MPI; 2002-627544/67.
DR P-PSDB; ABB79886.
XX
XX Novel hybridoma cell capable of producing monoclonal antibody G250, which
PT is useful in the treatment of renal cell carcinoma and metastases after
PT tumor surgery.
XX
XX Example 3; Fig 1; 20pp; English.
XX
XX The present sequence is the coding sequence for the heavy chain variable
CC region (VH) of murine monoclonal antibody (Mab) G250. The coding sequence
CC was obtained from a clone obtained by PCR amplification of hybridoma G250
CC (DSM ACC 2526) cDNA and cloning into vector pUC19. Mab G250 (IgG1)
CC recognises MN antigen, which is preferentially expressed on membranes of
CC renal cell carcinoma cells and not expressed in healthy proximal tubular
CC epithelium. The present invention relates to a hybridoma cell, and to progeny
CC specifically DSM ACC 2526, capable of producing Mab G250, and to progeny
CC cells produced e.g. by recombinant DNA methods. The invention also
CC relates to the use of the hybridoma cell and progeny cells for the
CC production of G250 antibodies, e.g. Mab, chimeric antibodies, (fully)
CC humanised antibodies, bispecific antibodies or chimeric antibodies,
CC especially radiolabelled chimeric antibodies or chimeric antibodies
CC coupled to a cytokine such as Interleukin-2, tumour necrosis factor
CC and/or granulocyte-macrophage colony stimulating factor. A chimeric G250
CC antibody was successfully used in clinical studies for the treatment of
CC renal cell carcinoma cells after surgery. In some cases, tumour
CC regression occurred more than 6 months after start of therapy. Thus,
CC chimeric G250 antibody and other G250 antibodies are capable of eliciting
CC a delayed immune response in cancer therapy, preferably in the treatment
CC of renal cell carcinoma and more preferably in the treatment of
CC metastases after tumour surgery
XX
XX
XX Sequence 357 BP; 86 A; 87 C; 94 G; 90 T; 0 U; 0 Other;
SQ

```

```

Alignment Scores:
Pred. No.: 1.12e-58 Length: 357
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

```

US-10-635-908-6 (1-119) x ABO81172 (1-357)

```

QY 1 AAPPVALLVLEUVALGUSERGIYGLIYLVALLVLEUVALYGLISERILEUVALLEN 20
DB 1 GACGTAAAGCTCTGAGAGTCTGGGGAGGCTTAGTAAAGCTTGGAGGGCTCCGAAATC 60
QY 21 SERYAALALASERGIYPhenrpheserSantYrTYrWeserTYrVALArginThr 40
DB 61 TCTGTGACAGCCCTGGATTCACTTTCAGTAATTAATTAATTAATTAATTAATTAAT 120
QY 41 ProGluYrAArgLeuGluLeuValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 60
DB 121 CCGAAGAAAGAGCTGAGAGTGTGGCAGCCATTAATAGTATGTGTATACACCTACTAT 180
QY 61 LeuAspThrValValysGIYrAArgPhenrThrIleSerArgAspAsnAlaLysAsnThrLeuYr 80
DB 181 CTAGACACTGTGAAGGCCGATTCACCATTTCAAGAGACAAATGCCAAGAACCCCTGTAC 240
QY 81 LeuGlnMetSerSerLeuYrSergIuAspThrAlaLeuPheTYrCYsAlaArgHisArg 100
DB 241 CTCGAATATGAGAGTCTGAGAGTCTGAGAGACACAGCCCTGTTTACTGTGCAAGACCGC 300
QY 101 SerGIYrYrPheserMetAspTYrTrpGIYrGlnGIYrThrSerValThrValSerSer 119

```

```

DB 301 TCGGGCTACTTTCTATGACTACTGGGCTCAAGAACTCAGTACCCGCTCTCTCA 357
RESULT 2
AB079691
ID AB079691 standard; DNA; 357 BP.
XX
XX AB079691;
XX
XX 05-DEC-2002 (first entry)
XX
XX G250 heavy chain variable region (VH G250) encoding DNA.
XX Antibody; antigen-binding site; diagnostic; therapeutic; radiolabeling;
XX cytotoxic; G250; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..357
XX FT /*tag= a
XX FT /product= "VH G250"
XX FT /partial
XX
XX MO200263010-A2.
XX
XX 15-AUG-2002.
XX
XX 07-FEB-2002; 2002WO-EP001283.
XX
XX 07-FEB-2001; 2001US-0266853P.
XX 05-OCT-2001; 2001US-0327008P.
XX
XX (WILE-) WILEX AG.
XX
XX Bolhuis RL, Weehl T, Boettger V;
XX MPI; 2002-627562/67.
XX P-PSDB; ABB82004.
XX
XX Novel nucleic acid sequence encoding antigen-binding site of the heavy or
PT light chain of an antibody useful for expressing the antibody suitable in
PT the field of tumor diagnostics and therapeutics.
XX
XX Claim 4; Fig 1; 18pp; English.
XX
XX The invention relates to novel nucleic acid (I) encoding the antigen-
CC binding site of the heavy or light chain of an antibody comprising a
CC nucleotide sequence encoding the CDR3 region. (I) is useful for the
CC recombinant production of a polypeptide having an antigen-binding site,
CC by introducing (I) into a mammalian cell, culturing the cell in a medium
CC where an expression of the nucleic acid takes place, and obtaining the
CC expressed product from the medium and/or the cell. Before introducing (I)
CC into the cell, the nucleic acid is modified so that the modification does
CC not alter the amino acid sequence of the antigen-binding site of the
CC polypeptide to be expressed. The expressed product, preferably antibodies
CC and antibody fragments are useful for preparing a diagnostic or
CC therapeutic agent and are coupled to a diagnostic marker or cytotoxic
CC agent. (I) is useful for expressing antibodies, e.g. chimerized
CC antibodies, humanized antibodies, heterobispecific antibodies, and single
CC chain antibodies, or antibody fragments. The expressed product can be
CC coupled to a diagnostic marker for use in in vitro diagnostic methods, or
CC radiolabeling procedures, or to a cytotoxic agent, e.g. a radionuclide, or
CC a toxin such as cholera toxin or ricin. The present sequence represents
CC G250 heavy chain variable region encoding DNA
XX
XX
XX Sequence 357 BP; 86 A; 87 C; 94 G; 90 T; 0 U; 0 Other;
SQ

```

```

Alignment Scores:
Pred. No.: 1.12e-58 Length: 357
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

```

Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0

US-10-635-908-6 (1-119) x ABQ79691 (1-357)

```
QY 1 AspVallylsLeuValGluSerGlyGlyLeuVallylsLeuGlyGlySerLeuValLeu 20
DB 1 GACGTGAAGCTCGTGAAGCTCGGGGAGGCTTAGTGAAGCTTGAGAGGCTCCGAAACCTC 60
QY 21 SerCyAlAlAAserylPheThrPheSerAsnTyrTyrMetSertPValArgGlnThr 40
DB 61 TCCGTGACACCCCTCGATTCACTTTCAGTAACTATTACATGCTTGGGTTCCGCAAGACT 120
QY 41 ProGluysArghLeuGluLeuValAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 60
DB 121 CCAGAGAGAGGCTGAGAGTGGTCGAGCATTATATGATGCTGTATCACCCTATAT 180
QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlAlAsanThrLeuTyr 80
DB 181 CTAGACACTGTGAAGGCCGATTCCACATTTCAAGAGACAATGCAAGAACACCCCTGTAC 240
QY 81 LeuGlnMetSerSerLeuLysSerGlyAspThrAlAlAlAlAlAlAlAlAlAlAlAlAl 100
DB 241 CTGCAATATGACAGCTGGAAGCTGAGAGACACGCTTGTATTACTGTGCAAGACACGC 300
QY 101 SerGlyTyrPheSerMetAspTyrTyrGlyGlnGlyThrSerValThrValSerSer 119
DB 301 TCGGGCTACTTTTCTATGACTACTGAGGCTCAGAGAACTCAGTACCGTCTCCTCA 357
```

RESULT 3

ABK43187 ID ABK43187 standard; DNA; 1056 BP.

AC ABK43187;

DT 05-JUN-2002 (first entry)

XX DNA encoding construct G250.

DE Modified virus; adenovirus; cytostatic; gene therapy; tumour cell;

KW proliferating cell; cancer; vascular disease; inflammatory disease;

KW infectious disease; human immunodeficiency virus; HIV; gene; de.

OS Human adenovirus type 5.

XX Synthetic.

XX WO200208263-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-GB003252.

XX 19-JUL-2000; 2000GB-00017720.

XX (GOTA-) GOT-A-GENE AB.

XX (GARD/) GARDNER R.

XX Lindholm L, Nord AK, Boulanger PA;

XX WPI; 2002-217049/27.

XX P-PSDB; AAU87031.

XX Novel modified virus comprising non-native polypeptides with stable

XX conformation and having framework moieties containing binding moieties

XX which confer upon the virus, an altered tropism, useful in gene therapy.

CC ligands for the binding moieties, where the conformation allows the

CC binding moiety subsequently to bind with the ligand. The modified virus

CC is useful in therapy for the preparation of a medicament for treating

CC tumour cells, cancer, proliferating cells, vascular diseases,

CC inflammatory diseases and infectious diseases such as Human

CC immunodeficiency virus (HIV). The altered tropisms allow the virus to be

CC used in treatment of, or ex vivo treatment of cells of, the subject

CC requiring treatment. The problems associated with the expression of

CC functional non-native viral components in the nucleus and cytosol of host

CC cells is solved by using the modified virus for the purpose. This

CC sequence encodes a protein sequence used in the creation of the modified

XX virus containing non-native polypeptides

SQ Sequence 1056 BP; 268 A; 285 C; 271 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4 02e-58	Length:	1056
Score:	617.00	Matches:	119
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-635-908-6 (1-119) x ABK43187 (1-1056)

```
QY 1 AspVallylsLeuValGluSerGlyGlyLeuVallylsLeuGlyGlySerLeuValLeu 20
DB 376 GACGTGAAGCTCGTGAAGCTCGGGGAGGCTTAGTGAAGCTTGAGAGGCTCCGAAACCTC 435
QY 21 SerCyAlAlAAserylPheThrPheSerAsnTyrTyrMetSertPValArgGlnThr 40
DB 436 TCCGTGACACCCCTCGATTCACTTTCAGTAACTATTACATGCTTGGGTTCCGCAAGACT 495
QY 41 ProGluysArghLeuGluLeuValAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 60
DB 496 CCAGAGAGAGGCTGAGAGTGGTCGAGCATTATATGATGCTGTATCACCCTATAT 555
QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlAlAsanThrLeuTyr 80
DB 556 CTAGACACTGTGAAGGCCGATTCCACATTTCAAGAGACAATGCAAGAACACCCCTGTAC 615
QY 81 LeuGlnMetSerSerLeuLysSerGlyAspThrAlAlAlAlAlAlAlAlAlAlAlAlAl 100
DB 616 CTGCAATATGACAGCTGGAAGCTGAGAGACACGCTTGTATTACTGTGCAAGACACGC 675
QY 101 SerGlyTyrPheSerMetAspTyrTyrGlyGlnGlyThrSerValThrValSerSer 119
DB 676 TCGGGCTACTTTTCTATGACTACTGAGGCTCAGAGAACTCAGTACCGTCTCCTCA 732
```

RESULT 4

ABK43189 ID ABK43189 standard; DNA; 1411 BP.

AC ABK43189;

DT 05-JUN-2002 (first entry)

XX DNA encoding fiber construct A1 G250.

XX Modified virus; adenovirus; cytostatic; gene therapy; tumour cell;

XX proliferating cell; cancer; vascular disease; inflammatory disease;

XX infectious disease; human immunodeficiency virus; HIV; gene; de.

XX Human adenovirus type 5.

XX Synthetic.

XX WO200208263-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-GB003252.

```
PR 19-JUL-2000; 2000GB-00017720.
XX
XX (GOTA-) GOT-A-GENE AB.
PA (GARD/) GARDNER R.
XX
XX Lindholm L, Nord AK, Boulanger PA;
PI WPI; 2002-217049/27.
XX P-PSDB; AAU87033.
DR
XX Novel modified virus comprising non-native polypeptides with stable
PT conformation and having framework moieties containing binding moieties
PT which confer upon the virus, an altered tropism, useful in gene therapy.
XX
XX Example 3; Page 104-109; 163pp; English.
XX
XX The invention describes a modified virus comprising non-native
CC polypeptides which has framework moieties each containing binding
CC moieties, where the virus has altered tropism conferred by the binding
CC moieties. The polypeptides can be expressed in the cytoplasm and nucleus
CC of mammalian host cell in conformation which is maintained in absence of
CC ligands for the binding moieties, where the conformation allows the
CC binding moiety subsequently to bind with the ligand. The modified virus
CC is useful in therapy for the preparation of a medicament for treating
CC tumour cells, cancer, proliferating cells, vascular diseases,
CC inflammatory diseases and infectious diseases such as Human
CC immunodeficiency virus (HIV). The altered tropisms allow the virus to be
CC used in treatment of disease in human or animal subjects, either by in
CC vivo treatment of, or ex vivo treatment of cells of, the subject
CC requiring treatment. The problems associated with the expression of
CC functional non-native viral components in the nucleus and cytosol of host
CC cells is solved by using the modified virus for the purpose. This
CC sequence encodes a protein sequence used in the creation of the modified
CC virus containing non-native polypeptides
XX
SQ Sequence 1411 BP; 363 A; 391 C; 349 G; 308 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 5.65e-58 Length: 1411
XX Score: 617.00 Matches: 119
XX Percent Similarity: 100.0% Conservative: 0
XX Best Local Similarity: 100.0% Mismatches: 0
XX Query Match: 100.0% Indels: 0
XX Gaps: 0
XX
XX US-10-635-908-6 (1-119) x ABK43190 (1-1411)
XX
XX 1 AspValIysLeuValGluSerGlyGlyLeuValIysLeuGlySerLeuLysLeu 20
DB 722 GACGTAAAGCTCGTGAAGCTGAGGAGGCTTAGTGAAGCTTGAGAGGTCCTGAAAC 781
XX
XX 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrrTyMetSerTrpValArgIntnr 40
DB 782 TCTCTGAGCAGCCTCGATTCACCTTCAGTAACATATACATGCTTGGGTTCCCGACAG 841
XX
XX 41 ProGluIysArgLeuGluIleuValAlaIleAsnSerAspGlyIleThrTyrrTy 60
DB 842 CCAGAGAAAGAGGTGAGAGTTGGTCGACGACATTAATGATGATGATGATGATGATGAT 901
XX
XX 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLys 80
DB 902 CTAGACACACTGTGAAGGCCGATTCACCATTTCAAGAGACAAATCCCAAGAACCCCTGAC 961
XX
XX 81 LeuGlnMetSerSerLeuIysSerGlyAspThrAlaLeuPheTyrrCyAlaArgHisArg 100
DB 962 CTGCAATATGAGCAGTCTGAAGTCTGAGGACACAGCCCTTGTTTACTGTCGAAGACAC 1021
XX
XX 101 SerGlyTyrrPheSerMetAspTyrrTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 1022 TCGGGCTACTTTCTATGAGCTACTGCGGAGCAAGAACCTCACTCCGCTCTCTCA 1078
XX
XX RESULT 5
XX ABK43190
```

```
ID ABK43190 standard; DNA; 1702 BP.
XX
XX AC ABK43190;
XX
XX 05-JUN-2002 (first entry)
XX
XX DE DNA encoding fiber construct A7 G250.
XX
XX KW Modified virus; adenovirus; cytostatic; gene therapy; tumour cell;
XX proliferating cell; cancer; vascular disease; inflammatory disease;
XX infectious disease; human immunodeficiency virus; HIV; gene; ds.
XX
XX OS Human adenovirus type 5.
XX
XX OS Synthetic.
XX
XX PN WO200208263-A2.
XX
XX PD 31-JAN-2002.
XX
XX PF 19-JUL-2001; 2001WO-GB003252.
XX
XX PR 19-JUL-2000; 2000GB-00017720.
XX
XX PA (GOTA-) GOT-A-GENE AB.
XX (GARD/) GARDNER R.
XX
XX PI Lindholm L, Nord AK, Boulanger PA;
XX WPI; 2002-217049/27.
XX P-PSDB; AAU87034.
XX
XX PT Novel modified virus comprising non-native polypeptides with stable
XX conformation and having framework moieties containing binding moieties
XX which confer upon the virus, an altered tropism, useful in gene therapy.
XX
XX Example 3; Page 109-116; 163pp; English.
XX
XX The invention describes a modified virus comprising non-native
CC polypeptides which has framework moieties each containing binding
CC moieties, where the virus has altered tropism conferred by the binding
CC moieties. The polypeptides can be expressed in the cytoplasm and nucleus
CC of mammalian host cell in conformation which is maintained in absence of
CC ligands for the binding moieties, where the conformation allows the
CC binding moiety subsequently to bind with the ligand. The modified virus
CC is useful in therapy for the preparation of a medicament for treating
CC tumour cells, cancer, proliferating cells, vascular diseases,
CC inflammatory diseases and infectious diseases such as Human
CC immunodeficiency virus (HIV). The altered tropisms allow the virus to be
CC used in treatment of disease in human or animal subjects, either by in
CC vivo treatment of, or ex vivo treatment of cells of, the subject
CC requiring treatment. The problems associated with the expression of
CC functional non-native viral components in the nucleus and cytosol of host
CC cells is solved by using the modified virus for the purpose. This
CC sequence encodes a protein sequence used in the creation of the modified
CC virus containing non-native polypeptides
XX
XX SQ Sequence 1702 BP; 447 A; 494 C; 404 G; 357 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 7.05e-58 Length: 1702
XX Score: 617.00 Matches: 119
XX Percent Similarity: 100.0% Conservative: 0
XX Best Local Similarity: 100.0% Mismatches: 0
XX Query Match: 100.0% Indels: 0
XX Gaps: 0
XX
XX US-10-635-908-6 (1-119) x ABK43190 (1-1702)
XX
XX 1 AspValIysLeuValGluSerGlyGlyLeuValIysLeuGlySerLeuLysLeu 20
DB 1013 GACGTAAAGCTCGTGAAGCTGAGGAGGCTTAGTGAAGCTTGAGAGGTCCTGAAAC 1072
XX
XX 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrrTyMetSerTrpValArgIntnr 40
```



```
DB 1073 TCCTGTGCACCTCTGGATTACCTTTCAGTACATATACATGCTTGGGTTCCCGAGACT 1132
QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
DB 1133 CCAGAGAAAGAGGCTGGAGTTGGTCGCGACCATTAATGTATGATGGTATACCTACTAT 1192
QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
DB 1193 CTAGACACTGTGAAGGCCCATTCACATTCAGAGACAAATGCCAAGAACCCCTGTAC 1252
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
DB 1253 CTGCAATATGACAGTCTGAAGTCTGAGACACACCCCTGTTTACTGTGCAGACACCGC 1312
QY 101 SerGlyTyrPheSerMetAspTyrTTPGlyGlnGlyThrSerValThrValSerSer 119
DB 1313 TCGGGCTACTTTTCTATGACTACTGGGCTCAAGAACCTCAGTCACCGTCTCTCA 1369
RESULT 6
ADC24965
ID ADC24965 standard; DNA; 444 BP.
XX AC ADC24965;
XX DT 18-DEC-2003 (first entry)
XX DE Murine G250 heavy chain variable region DNA SEQ ID NO:50.
XX KW fusion protein; chimerised antibody; tumour necrosis factor; TNF;
KW antibody; chimeric fusion protein; antiinflammatory; antirheumatic;
KW antiarthritic; antipsoriatic; antiaesthetic; neuroprotective; vincristine;
KW antineoplastic; immunosuppressive; nephrotoxic; antiarteriosclerotic;
KW rheumatoid arthritis; inflammatory condition; psoriasis; asthma;
KW inflammatory bowel disease; multiple sclerosis; viral pneumonia;
KW bacterial pneumonia; septic shock; nephritis; arteriosclerosis; mouse;
KW gene; ds.
XX OS Synthetic.
XX MU Mus sp.
XX PN WO2003068924-A2.
XX PD 21-AUG-2003.
XX PF 12-FEB-2003; 2003WO-US004243.
XX PR 13-FEB-2002; 2002US-0355838P.
XX RA (LUDW-) LUDWIG INST CANCER RES.
XX PI Renner C, Scott A;
XX DR WPI; 2003-679629/64.
XX DR P-PSDB; ADC24966.
XX PT New nucleic acid, useful for producing humanized or chimeric antibodies,
XX PT or fusion proteins comprising the antibodies, which are G250-specific and
XX PT useful for treating inflammatory conditions, e.g. Rheumatoid arthritis or
XX PT asthma.
XX PS Example 16; SEQ ID NO 50; 80pp; English.
XX CC The present invention describes an isolated nucleic acid molecule, which
XX CC encodes a fusion protein comprising a chimerised antibody molecule, and a
XX CC tumour necrosis factor (TNF) molecule or its fragment. The antibody
XX CC specifically binds to a target. The fragment of the TNF molecule
XX CC possesses the cell killing properties of a full-length TNF molecule. Also
XX CC described: (1) a chimeric fusion protein (I) encoded by the isolated
XX CC nucleic acid molecule; (2) an expression vector comprising the isolated
XX CC nucleic acid molecule operably linked to a promoter; and (3) a
XX CC recombinant cell comprising the isolated nucleic acid molecule or the
XX CC expression vector. (I) has antiinflammatory, antirheumatic,
```

```
CC antiarthritic, antipsoriatic, antiaesthetic, neuroprotective, vincristine,
CC antibacterial, immunosuppressive, nephrotoxic and antiarteriosclerotic
CC activities. The nucleic acid is useful for the expression of proteins,
CC especially antibodies, as well as fusion proteins that incorporate the
CC antibody and a protein. The expression vector is useful in manufacturing
CC a recombinant antibody (e.g. a fully human, humanized or chimeric
CC antibody) in a eukaryotic cell. The antibody is useful in therapy,
CC particularly for targeting G250 and blocking granulocyte-macrophage
CC stimulating factor (GM-CSF), which is involved in the development of
CC rheumatoid arthritis. The antibody is useful for treating inflammatory
CC conditions, e.g. psoriasis, asthma, inflammatory bowel disease, multiple
CC sclerosis, viral or bacterial pneumonia, septic shock, nephritis, or
CC arteriosclerosis. The present sequence encodes murine G250 antibody heavy
CC chain variable region, which is used in an example from the present
CC invention.
XX SQ Sequence 444 BP; 103 A; 108 C; 114 G; 119 T; 0 U; 0 Other;
XX Alignment Scores:
XX Pred. No.: 3e-57 Length: 444
XX Score: 605.00 Matches: 117
XX Percent Similarity: 98.3% Conservative: 0
XX Best Local Similarity: 98.3% Mismatches: 2
XX Query Match: 98.1% Indels: 0
XX DB: Gaps: 10
XX US-10-635-908-6 (1-119) x ADC24965 (1-444)
QY 1 AspVallyshLeuValGluSerGlyGlyLeuVallyshLeuVallyshLeuVallyshLeu 20
DB 75 GAGGTGAAGTCTGGAAGTCTGGGCGAGCTTGTGAAGCTTGGAGGCTCCGTGAATC 134
QY 21 SerCysAlaIleAsnSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgIleThr 40
DB 135 TCCTGTGCACCTCTGGATTACCTTTCAGTACATATACATGCTTGGGTTCCCGAGACT 194
QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
DB 195 CCAGAGAAAGAGGCTGGAGTTGGTCGCGACCATTAATGTATGATGGTATACCTACTAT 254
QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
DB 255 CTAGACACTGTGAAGGCCCATTCACATTCAGAGACAAATGCCAAGAACCCCTGTAC 314
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
DB 315 CTGCAATATGACAGTCTGAAGTCTGAGACACACCCCTGTTTACTGTGCAGACACCGC 374
QY 101 SerGlyTyrPheSerMetAspTyrTTPGlyGlnGlyThrSerValThrValSerSer 119
DB 375 TCAGCTACTTTTCTATGACTACTGGGCTCAAGAACCTCAGTCACCGTCTCTCA 431
RESULT 7
ADK51720
ID ADK51720 standard; DNA; 444 BP.
XX AC ADK51720;
XX DT 06-MAY-2004 (first entry)
XX DE Murine G250 variable heavy chain region cDNA.
XX KW granulocyte macrophage colony stimulating factor; GM-CSF; antibody;
XX KW antiinflammatory; antirheumatic; antirheumatic; rheumatoid arthritis;
XX KW inflammatory disease; murine; mouse; G250; gene; ss.
XX OS Mus sp.
XX PN WO2003068920-A2.
XX PD 21-AUG-2003.
XX PF 12-FEB-2003; 2003WO-US004185.
```

PR	XX	13-FEB-2002; 2002US-0355838P.
XX	PA	(LUDW-) LUDWIG INST CANCER RES.
XX	PI	Renner C, Scott A, Burgess A;
XX	PS	WPI; 2003-679625/64.
DR	P-RSDB;	ADK51721.
XX	PT	Nucleic acids encoding chimeric granulocyte macrophage colony stimulating factor (GM-CSF) specific antibodies comprising a light and a heavy chain, useful for blocking effects of GM-CSF on cells, e.g. in preventing rheumatoid arthritis.
XX	PS	Example 16; SEQ ID NO 50; 81bp; English.
XX	CC	The invention relates to an isolated nucleic acid encoding a chimerised granulocyte macrophage colony stimulating factor (GM-CSF) specific antibody light chain or heavy chain. The invention further relates to: a chimerised granulocyte macrophage colony stimulating factor (GM-CSF) specific antibody light chain encoded by nucleotides 1357-1752 of a defined sequence of 6159 bp concatenated to the amino acid sequence encoded by nucleotides 186-2203 of the 6159bp sequence; or a chimerised GM-CSF specific antibody heavy chain encoded by nucleotides 1357-1764 of a defined 6629 bp sequence concatenated to the amino acid sequence encoded by nucleotides 1839-2825 of the 6629bp sequence. The GM-CSF antibodies have antiinflammatory, antiarthritic, and antirheumatic activities. The GM-CSF nucleic acid is useful for blocking GM-CSF and its effects on cells, such as in preventing the development of rheumatoid arthritis and other inflammatory diseases and conditions. This polynucleotide sequence represents the cDNA of a murine G250 heavy chain variable region protein of the invention.
XX	SQ	Sequence 444 BP; 103 A; 108 C; 114 G; 119 T; 0 U; 0 Other;
XX	Alignment Scores:	
	Pred. No.:	36-57 Length: 444
	Score:	605.00 Matches: 117
	Percent Similarity:	98.3% Conservative: 0
	Best Local Similarity:	98.3% Mismatches: 2
	Query Match:	98.1% Indels: 0
DB:	Gaps:	0
US-10-635-908-6 (1-119) x ADK51720 (1-444)		
OY	1	AAPVALYLEUVAIGLSERGIGLYGLEUVALLYSLEUNGILGYSERILEUVALEU 20
Db	75	GACGTGAAGCTCGTGAGTCTGGGCAAGCCTTAGTGAAGCTTGAGGGTCCCTGAATCTC 134
OY	21	SERCYSAIAAISERICLYPHERTHRPRESERTARTTYTMETSEITPVALAAGINTHR 40
Db	135	TCCCTGTGCAGCCTCTGGATTCACTTCAGTAATCATTAATGCTTTGGGTGCCAGACT 194
OY	41	PROGILYVARYLEUGILUEUVALAIAAIIAESERSASPGLYLITHTRTYTYR 60
Db	195	CCAAGAAGAGAGCTGAGTGTGGCGCAGCCATTAAATGATCATGTGTGATCACCTACTAT 254
OY	61	LEUAAPTTRVALLYEGIYARGPHERHRLIESERARASPSANALALYSABANTRLUETR 80
Db	255	CTAGACACACTGTAAAGGCGCATTCACCATTTCAAGAGACATCCCAAAGAACACCCTGTAC 314
OY	81	LAUGIMETSERSERILEUYSSERGIUNAPTTRVALALEUPHERTYCYSAIAATRGHISARG 100
Db	315	CTGCATAATAGCAAGTCTGAAGTCTGAGACACAGCCCTGTATTACATGTCAGCAAGCACCCG 374
OY	101	SERGIYTYRPHESERMETAPRYTTPGILYINGILYTHSERVALTHVALSERSER 119
Db	375	TCAGGCTACTTTTCTATGACTACTAGGGGTCAAGAACTCAGTTCACCGTCTCTCA 431
RESULT 8		
ID	ABO79699	standard; DNA; 2431 BP.

XX		AC	ABQ79699;	
XX		AC		
DT		05-DEC-2002	(first entry)	
DE		G250 heavy chain variable region (HC_G250) DNA fragment.		
XX				
KM		Antibody; antigen-binding site; diagnostic; therapeutic; radiomaging;		
XX		Cytotoxic; G250; ds.		
OS		Homo sapiens.		
XX				
PN		W0200263010-A2.		
XX				
PD		15-AUG-2002.		
PF		07-FEB-2002; 2002WO-EP001283.		
XX				
PR		07-FEB-2001; 2001US-0266853P.		
XX		05-OCT-2001; 2001US-0327008P.		
PA		(WILEY-) WILEX AG.		
PI		Bolhuis RL, Wehl T, Boettger V;		
DR		WPI; 2002-627562/67.		
XX				
PT		Novel nucleic acid sequence encoding antigen-binding site of the heavy or		
PT		light chain of an antibody useful for expressing the antibody suitable in		
XX		the field of tumor diagnostics and therapeutics.		
PS		Example 2; Fig 3A; 18pp; English.		
XX		The invention relates to novel nucleic acid (I) encoding the antigen-		
CC		-binding site of the heavy or light chain of an antibody comprising a		
CC		nucleotide sequence encoding the CDR3 region. (I) is useful for the		
CC		recombinant production of a polypeptide having an antigen-binding site,		
CC		by introducing (I) into a mammalian cell, culturing the cell in a medium		
CC		where an expression of the nucleic acid takes place, and obtaining the (I)		
CC		expressed product from the medium and/or the cell. Before introducing (I)		
CC		into the cell, the nucleic acid is modified so that the modification does		
CC		not alter the amino acid sequence of the antigen-binding site of the		
CC		polypeptide to be expressed. The expressed product, preferably antibodies		
CC		and antibody fragments are useful for preparing a diagnostic or		
CC		therapeutic agent and are coupled to a diagnostic marker or cytotoxic		
CC		agent. (I) is useful for expressing antibodies, e.g. chimerized		
CC		antibodies, humanized antibodies, heterobispecific antibodies, and single		
CC		chain antibodies, or antibody fragments. The expressed product can be		
CC		coupled to a diagnostic marker for use in in vitro diagnostic methods,		
CC		radiomaging procedures, or to a cytotoxic agent, e.g. a radionuclide, or		
CC		a toxin such as cholera toxin or ricin. The present sequence represents		
CC		G250 heavy chain variable region DNA fragment HC_G250 (BCORI-Fragment in		
XX		expression vector)		
SQ		Sequence 2431 BP; 720 A; 455 C; 552 G; 698 T; 0 U; 6 Other;		
Alignment Scores:				
Pred. No.:	1_31e-55	Length:	2431	
Score:	598.00	Matches:	115	
Percent Similarity:	97.5%	Conservative:	1	
Best Local Similarity:	96.6%	Mismatches:	3	
Query Match:	96.9%	Indels:	0	
DB:	6	Gaps:	0	
UY	10-10-635-908-6 (1-119) x ABQ79699 (1-2431)			
Dy	1 AspValLysLeuValGlnSerGlyGlyLeuValLysLeuGlyGlySerLeuLysLeu 20			
Dd	843 GAGGTGAAGACTCGTAGGAGCTGGGGGAGGAGCTTAAAGAAGTTGAGGGTCCTGAAAATC 902			
Oy	21 SerCyAlAlAsSerGlyPheThrPheSerAnrTYrMetSerTPVAlArgInThr 40			
Dd	903 TCCTGGACAGCCTTGGAATTCACTTCAGTAACATATTCAGTCTTGAGTTGCCAACACT 962			

```

QY 41 ProGluLyAArgLeuGluLeuValAlaAlaIleasnSerAspGlyGlyIleThrTyTyTyr 60
Db 963 CCAGAGAGAGGCTGGAGTTGGTCGCANNATTAANNNTGATGGTGTATCAGCTTACT 1022
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyTyr 80
Db 1023 CTAGACACTGTGAGAGGCCGATTACCATTTCAAGAGACAATGCCAAGAACACCTGTATC 1082
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyTyrCysAlaArgHisArg 100
Db 1083 CTCGAATATGACGAGCTGGAAGCTCGAGACACAGCCCTGTGTTTACCTGTGCAAGACACCGC 1142
QY 101 SerGlyThrPheSerMetAspTyTyrTrpGlyGlnGlyThrSerValThrValSerSer 119
Db 1143 TCGGGCTACTTTCATTCAGCACTACTGCGGGTCAGAGAACCTTCAGTCACTGCTCTCTCA 1199

RESULT 9
AAT70808
ID AAT70808 standard; DNA; 474 BP.
AC AAT70808;
DT 30-JUL-1997 (first entry)
XX
DE Mouse anti-idiotypic antibody 3B6 heavy chain variable region.
KM Anti-idiotypic; anti-BGFR; epidermal growth factor receptor; tumour;
KW cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 1..474
FT /*tag= a
FT /transl_except= pos:388..390, aa: Ala
FT /note= "no stop codon given"
FT sig_peptide 1..57
FT /*tag= b
FT primer_bind 1..30
FT /*tag= c
FT primer_bind 448..474
FT /*tag= d
XX
PN EP745612-A1.
XX
PD 04-DEC-1996.
XX
PF 14-MAY-1996; 96EP-00107651.
XX
PR 26-MAY-1995; 95EP-00107967.
XX
PA (MERCK ) MERCK PATENT GMBH.
XX
PI Carceller A, Rosell E, Gomez A, Adan J, Piuilats J;
XX
DR WPI, 1997-013659/02.
DR P-PSDB; AAM19577.
XX
PT Monoclonal anti-idiotypic antibodies mimicking epidermal growth factor
PT receptor - useful for tumour therapy.
XX
PS Claim 6; Fig 5C; 28pp; English.
XX
CC Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are new.
CC They induce an immune response against epidermal growth factor receptor
CC (EGFR). The sequences of the heavy and light chain variable regions of
CC these antibodies are given in the specification. The antibodies are used
CC for the manufacture of drugs directed against tumours that express EGFR
CC on their surface, including melanomas, gliomas and carcinomas
XX
SQ Sequence 474 BP; 112 A; 119 C; 122 G; 121 T; 0 U; 0 Other;

```

```

Alignment Scores:
Pred. No.: 1.7e-52 Length: 474
Score: 562.00 Matches: 112
Percent Similarity: 92.8% Conservative: 4
Beet Local Similarity: 89.6% Mismatches: 3
Query Match: 91.1% Indels: 6
DB: 2 Gaps: 2

US-10-635-908-6 (1-119) x AAT70808 (1-474)
QY 1 AspvallLyLeuValGluSerGlyGlyLeuValIysLeuGlyIleSerLeuLysLeu 20
Db 58 GACGTAAAGCTCGTGAAGTGGGGAGCTTAGTAAGCTTGAGAGGTCCTGGAATC 117
QY 21 SerCysAlaIleSerGlyPheThrPheSerAsnTyTyrMetSerTrpValArgGlnThr 40
Db 118 TCCGTGCGAGCCCTTGATTCATCTTCAGTAATTAATGCTGCTGGGTCCGAGACT 177
QY 41 ProGluLyAArgLeuGluLeuValAlaAlaIleasnSerAspGlyGlyIleThrTyTyTyr 60
Db 178 CCAGAGAGAGGCTGGAGTTGGTCGACGACCATTAATAGTAATGTTGTAGACACTTAT 237
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyTyr 80
Db 238 CCAGACACTGTGAGAGGCCGATTACCAATCTCCAGAGACAATGCCAAGAACACCTGTAC 297
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyTyrCysAlaArgHisArg 100
Db 298 CTCGAATATGACGAGCTGGAAGCTCGAGACACAGCCCTGTGTTTACCTGTGCAAGACATCGG 357
QY 101 -----SerGlyTyTyr-----PheSerMetAspTyTyrTrpGlyGlnGlyThrSer 114
Db 358 GCGAGGAGACAGCTCGGGCTTACGTAGGGTATTTATAGACTACGCGGTCAAGGAACCTCA 417
QY 115 ValThrValSerSer 119
Db 418 GTACCGCTCTCTCA 432

RESULT 10
AAT70810
ID AAT70810 standard; DNA; 474 BP.
AC AAT70810;
DT 30-JUL-1997 (first entry)
XX
DE Mouse anti-idiotypic antibody 5A6 heavy chain variable region.
XX
KM Anti-idiotypic; anti-BGFR; epidermal growth factor receptor; tumour;
KW cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 1..474
FT /*tag= a
FT /note= "no stop codon given"
FT sig_peptide 1..57
FT /*tag= b
FT primer_bind 1..25
FT /*tag= c
FT primer_bind 448..474
FT /*tag= d
XX
PN EP745612-A1.
XX
PD 04-DEC-1996.
XX
PF 14-MAY-1996; 96EP-00107651.
XX
PR 26-MAY-1995; 95EP-00107967.
XX
PA (MERCK ) MERCK PATENT GMBH.

```

XX Carceller A, Rosell E, Gomez A, Adan J, Piulats J;  
XX WPI; 1997-013659/02.  
DR P-P8DB; AAM19579.  
XX  
XX Monoclonal anti-idiotypic antibodies mimicking epidermal growth factor  
PT receptor - useful for tumour therapy.  
XX  
XX Claim 6; Fig 5E; 28pp; English.  
XX  
XX Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are new.  
CC They induce an immune response against epidermal growth factor receptor  
CC (EGFR). The sequences of the heavy and light chain variable regions of  
CC these antibodies are given in the specification. The antibodies are used  
CC for the manufacture of drugs directed against tumours that express EGFR  
CC on their surface, including melanomas, gliomas and carcinomas  
XX  
SQ Sequence 474 BP; 110 A; 117 C; 125 G; 122 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3.63e-52 Length: 474  
Score: 559.00 Matches: 111  
Percent Similarity: 92.8% Conservative: 5  
Best Local Similarity: 80.8% Mismatches: 3  
Query Match: 90.6% Indels: 6  
DB: Gaps: 2

US-10-635-908-6 (1-119) x AAT70810 (1-474)

QY 1 AspValIysLeuValAlGluSerGlyGlyLeuValIysLeuGlyIysSerLeuLysLeu 20  
DB 58 GACGTAAAGCTCTGAGAGCTGAGGAGAGCTTGTAAAGCTTGAGAGGCTCCGAAACAT 117  
QY 21 SerCyAlAlAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTryValArgGlnThr 40  
DB 118 TCCTGTGACAGCTCTGAGATTCACTTCAGTAATTAATTAATTAATTAATTAATTAATTA 177  
QY 41 ProGluIysArgLeuGluLeuValAlAlaIleAsnSerAspGlyIyleThrTyrTyr 60  
DB 178 CCAGAAAGAGGCTGAGAGTGTGCGAGCCATTAAATGTAATGTAATGTAATGTAATGTAAT 237  
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80  
DB 238 CCAGACACTGTGAAGGCCGATTCACCATCTCCAGAGCAATGCCAAGAACCCCTGTAC 297  
QY 81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTyrCyAlaArgHisArg 100  
DB 298 CTGCAATGAGAGCTGGAAGTCTGAGAGACACAGCCCTTGATTAATGTAATGTAATGTAAT 357  
QY 101 -----SerGlyTyr-----PheSerMetAspTyrTrpGlyGlnGlyThrSer 114  
DB 358 GGGAGGAGACAGCTCGGGCTTACGTAGGGTATGCTATGACTACTGGGCTCAAGGAACCTCA 417  
QY 115 ValThrValSerSer 119  
DB 418 GTCAACCGTCTCTCTCA 432

RESULT 11

AAC90629 ID AAC90629 standard; DNA; 422 BP.

XX AAC90629;

XX 20-MAR-2001 (first entry)

XX Plasmid gamma1WT-TAC sequence.

XX Somatic transgene immunisation; immune response; haematopoietic cell;

XX immunity; disease treatment; disease prevention; ds.

XX Synthetic.

PN WO20064488-A2.

XX 02-NOV-2000.

XX 27-APR-2000; 2000WO-US011372.

XX 27-APR-1999; 99US-00300959.

XX (ZANE/) ZANETTI M.

XX Zanetti M;

XX WPI; 2001-024628/03.

PT Immunization by administering ex vivo a transgene having a hematopoietic  
cell-specific expression element operationally linked to a polynucleotide  
encoding one or more heterologous epitopes to a lymphoid cell.

XX Example 1; Fig 2; 100pp; English.

CC The present invention provides a novel method of immunisation involving  
CC the administration of a haematopoietic cell specific expression element  
CC to a lymphoid cell. The method is known as somatic transgene  
CC immunisation. It is particularly useful in the treatment and prevention  
CC of tumours, autoimmune diseases, allergy, metabolic disorders, endocrine  
CC disorders, mental disorders, pain, blood disorders and dental disorders  
XX  
SQ Sequence 422 BP; 103 A; 98 C; 110 G; 111 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2.91e-49 Length: 422  
Score: 532.00 Matches: 106  
Percent Similarity: 90.8% Conservative: 2  
Best Local Similarity: 89.1% Mismatches: 11  
Query Match: 86.2% Indels: 0  
DB: Gaps: 0

US-10-635-908-6 (1-119) x AAC90629 (1-422)

QY 1 AspValIysLeuValAlGluSerGlyGlyLeuValIysLeuGlyIysSerLeuLysLeu 20  
DB 1 GACGTAAAGCTCTGAGAGCTGAGGAGAGCTTGTAAAGCTTGAGAGGCTCCGAAACAT 60  
QY 21 SerCyAlAlAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTryValArgGlnThr 40  
DB 61 TCCTGTGACAGCTCTGAGATTCACTTCAGTAATTAATTAATTAATTAATTAATTAATTA 120  
QY 41 ProGluIysArgLeuGluLeuValAlAlaIleAsnSerAspGlyIyleThrTyrTyr 60  
DB 121 CCAGAAAGAGGCTGAGAGTGTGCGAGCCATTAAATGTAATGTAATGTAATGTAATGTAAT 180  
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80  
DB 181 CCACACACTGTGAAGGCCGATTCACCATCTCCAGAGCAATGCCAAGAACCCCTGTAC 240  
QY 81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTyrCyAlaArgHisArg 100  
DB 241 CTGCAATGAGAGCTGGAAGTCTGAGAGACACAGCCCTTGATTAATGTAATGTAATGTAAT 300  
QY 101 SerGlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 119  
DB 301 CCTACTCTCATGTGATGACTACTGGGCTCAAGGAACCTCAGTCAACCGTCTCTCA 357

RESULT 12

AAT91614 ID AAT91614 standard; CDNA to mRNA; 735 BP.

XX AAT91614;

XX 22-DEC-1997 (first entry)

XX CDNA encoding an anti-T3 antibody derived scFv.

XX

XX	Single chain Fv; scFv; antibody; E. coli; anti-T3 antibody;
KM	anti-gp130 antibody; inclusion body; chaperonin; ds.
XX	Synthetic.
OS	
XX	
XX	Key
XX	Location/Qualifiers
FT	1..735
FT	/+tag= a
FT	/transl_except= pos:160..173, aa:TYR
FT	/transl_except= pos:385..387, aa:Glu
FT	/note= "No stop codon given"
XX	
XX	JF09220092-A.
XX	
XX	26-AUG-1997.
XX	
XX	15-FEB-1996; 96JP-00027622.
XX	
XX	15-FEB-1996; 96JP-00027622.
XX	
XX	(TOYO ) TOSOH CORP.
XX	
XX	WPI; 1997-474306/44.
DR	P-PsDB; AAM25783.
XX	
XX	Producing single chain Fv antibody in Escherichia coli - by expression in
PT	an inclusion body, followed by protein folding or by co-expression with a
PT	chaperonin as a soluble fraction.
XX	
XX	Claim 3; Page 5-6; 9pp; Japanese.
PS	
XX	The sequences given in AAT91614-15 encode single chain Fv (scFv)
CC	antibodies which are produced in E.coli. The scFv's are derived from an
CC	anti-T3 antibody or an anti-gp130 antibody and are produced either by:
CC	(1) expression as an inclusion body, followed by folding (i.e. by
CC	denaturation and solubilisation) or (2) expression as a soluble fraction
CC	by co-expression with chaperonin. Using the methods, scFv can be produced
CC	in E. coli, either in a soluble fraction or in inclusion bodies. Like the
CC	parent double chain antibodies, the scFv polypeptides are useful in
CC	immunological diagnosis or for separation and purification, but they
CC	lessen the side effects caused by antibody constant regions. The
CC	availability of scFv polypeptides contributes to fundamental research and
CC	development of diagnostic and therapeutic drugs
XX	
XX	Sequence 735 BP; 165 A; 192 C; 197 G; 181 T; 0 U; 0 Other;
SQ	
XX	
XX	Alignment Scores:
XX	Pred. No.: 6, 81e-47 Length: 735
XX	Score: 513.00 Matches: 103
XX	Percent Similarity: 90.1% Conservative: 6
XX	Best Local Similarity: 85.1% Mismatches: 10
XX	Query Match: 83.1% Indels: 2
DB:	Gaps: 1
DB:	
DB:	US-10-635-908-6 (1-119) x AAT91614 (1-735)
QY	1 AspValIysLeuValGluSerGlyGlyLeuValIysLeuGlyGlySerLeuYsLeu 20
DB	373 GAGGTCAAGCTGAGAGAGTCTGGGGAGGTTAGTGAAGTTGGCGGTCCTCGAAGACT 432
QY	21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyTyrIleMetSerTrpValArgGlnThr 40
DB	433 TCCTGTGAAGCCCTCTGATTCACCTTCACAGTACTATATACATGCTGCTGGGTTCCGCACAGACT 492
QY	41 ProGlnIlyArgGlnGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
DB	493 CCAGAGAAAGGGCTGGAGTGTGTGCGAGCCATTATATGATGATGGTATACCACTTACTAT 552
QY	61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80
DB	553 TCAGACACTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCAAGAACACCCGTAC 612
QY	81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTyrCysAlaIghIbArg 100

D6	613	CTGCAGAAATGACGACTGTAAGTCTGAGGACACACGCTTGATTAATCTGTGCAAGCCCGCTC	672
QY	101	serGlyTyr-----PheSerMetAspTyrTrpGlyGlnGlyThrSerValThrValSer	118
D6	673	TCTTATTATTACTCTCATGTCTATGTCTATGTAATCTACTGAGGCCACAGGACACGCTACCGTCTCC	732
QY	119	Ser 119	
Db	733	TCA 735	
RESULT 13			
ID	AAT71325	standard; cDNA to mRNA; 363 BP.	
AC	AAT71325;		
XX			
XX	12-SEP-1997	(first entry)	
XX			
DE		Thyroid hormone specific antibody TTI heavy chain variable region.	
XX			
KM		Thyroid hormone; antibody; heavy chain; light chain; variable region;	
XX		hybridoma; detection; ss.	
OS		Homo sapiens.	
XX			
PH	Key	Location/Qualifiers	
FT	CDS	1..357	
XX		/*tag= a	
XX		/note= "no start or stop codon given"	
PN	JP09107972-A.		
XX			
PD	28-APR-1997.		
XX			
PP	23-OCT-1995;	95JP-00274012.	
XX			
PR	23-OCT-1995;	95JP-00274012.	
XX			
XX	(TOYJ )	TOSOH CORP.	
PA			
XX	WPI; 1997-292465/27.		
DR	P-PSDB; AAW22515.		
XX			
PT	Gene fragment encoding thyroid hormone-recognising antibody - either the heavy or light chain variable region, recognises two different thyroid hormones.		
PS	Claim 1; Page 5-6; 7pp; Japanese.		
XX			
CC	AA771325 shows a cDNA sequence that encodes the heavy chain variable region of thyroid hormone specific TTI. A hybridoma producing TTI was created and used for TTI production. Antibody fragments are useful for identifying thyroid hormones. The hybridoma can be used to prepare the antibody having various additional functions in a large amount		
CC			
XX			
SQ	Sequence 363 BP; 87 A; 93 C; 93 G; 90 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	4.92e-47	Length: 363	
Score:	511.00	Matches: 103	
Percent Similarity:	90.0%	Conservative: 5	
Best Local Similarity:	85.8%	Mismatches: 10	
Query Match:	82.8%	Indels: 2	
DB:	2	Gaps: 1	
US-10-635-908-6 (1-119) X AAT71325 (1-363)			
QY	2	VallysleuVal]GluSerGlyGlyGlyLeuValylLeuGlyGlySerleuYsleuSer	21
Db	4	GTCACGCTGCACGGAGTCCTGGGGAGGCTTAGTGAAAGCTTGGCGGCTCCGTAAGAACTCTC	63
QY	22	CysAlaIaIaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThrPro	41

```

DB      64 TGTGAAGCCTCGATTCAGTTCATTTACATGCTTGGGTCGCAGACTCCA 123
      |||
QY      42 GIUYSARGLEUGLNUDEVALAIAIAIEANSEAPG1YGI1LETHRYTYRLEU 61
      |||
DB      124 GAGAAAGGCTGAGTGTGTCAGGCATTATAGTAATGTGTACCACTACTATTCA 183
      |||
QY      62 AAPTTHVALLEG1YARGPHERTH1LESERARGAPASNA1ALYSANThrLeuYrLeu 81
      |||
DB      184 GACACTGTGAAGGCCGATTCACATCTCCAGAGCAATGCCAAGAACACCCGTACTCG 243
      |||
QY      82 GINMESErSerLeuYsSerGIuAePTThrAlaLeuPheTYrCYeAlaArgHISArgSer 101
      |||
DB      244 CAAATGAGCAGTCTGAAGTCTGAGACACAGCCTGTATTACTGTGCCAAGCCGGTCTCC 303
      |||
QY      102 G1YTYR-----PheserMeTAePTTYrTPGIYGINGIYThrSerValThrValSerSer 119
      |||
DB      304 TTATTATTACCTCATGTCTACTGACTGAGGCGCAAGGAGCACGCTCACCGTCTCTCA 363
      |||

RESULT 14
AAV11906 standard; cDNA to mRNA, 354 BP.
XX
AC      AAV11906;
XX
DT      13-AUG-1998 (first entry)
XX
DE      Mouse PAF receptor antibody heavy chain hypervariable region cDNA.
XX
KW      Immunoglobulin heavy chain; hypervariable region; PAF; CDR; antibody;
XX      platelet activating factor receptor; murine; ds.
XX
OS      Mus sp.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..354
FT      FT      /*tag= a
FT      FT      /codon_start= 3
FT      FT      /product= "PAF receptor antibody heavy chain
FT      FT      hypervariable region"
FT      FT      /note= "partial coding sequence"
XX
PN      JP10136981-A.
XX
PD      26-MAY-1998.
XX
PF      12-NOV-1996; 96JP-00317047.
XX
PR      12-NOV-1996; 96JP-00317047.
XX
PA      (SUME ) SUMITOMO ELECTRIC IND CO.
XX
DR      WPI, 1998-355043/31.
XX      P-PSDB; AAMS9167.
XX
PT      Polypeptide comprising variable region of antibody recognising PAF
XX      receptor - useful for the preparation of chimeric antibody.
XX
PS      Disclosure; Page 8; 14pp; Japanese.
XX
CC      This sequence encodes the heavy chain hypervariable region of an antibody
CC      recognising the platelet activating factor (PAF) receptor. The variable
CC      region of mouse anti-PAF receptor monoclonal antibody is useful for the
CC      preparation of chimeric antibodies
XX
SQ      Sequence 354 BP; 88 A; 83 C; 95 G; 88 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      4.64e-46      Length:      354
Score:          502.00      Matches:      99
Percent Similarity: 89.7%      Conservative: 6
Best Local Similarity: 84.6%      Mismatches: 12
Query Match:    81.4%      Indels:      0

```

```

DB:      2      Gaps:      0
US-10-635-908-6 (1-119) x AAV11906 (1-354)
QY      2 VALLYSLEUVALIGUSERGIYGI1YLEUVALYLSLEUGLYG1YSERLEUYSLEUSER 21
      |||
DB      3 GTGAAGCTCCAGAGAGTCTGGGGAGGCTTAGGAAACTTGGAGGGTCCCTTAAACTCTCC 62
      |||
QY      22 CYeAlaIaISerGIYpHeThrPheSerANtYTYrMeTSerTYrValArgGlnThrPro 41
      |||
DB      63 TGTGACGCTCGATTCAGTTCATTTACATGCTTGGGTCGCAGACTCCA 122
      |||
QY      42 GIUYSARGLEUGLNUDEVALAIAIAIEANSEAPG1YGI1LETHRYTYRLEU 61
      |||
DB      122 GAGAAAGGCTGAAATGTGTCAGCCATTAATAGTAATGTGATPAACACTACTATCCA 182
      |||
QY      62 AAPTTHVALLEG1YARGPHERTH1LESERARGAPASNA1ALYSANThrLeuYrLeu 81
      |||
DB      183 GACAAATGTAAGGCGCGATTCACCATCTCCAGAGCAATGCCAAGAACACCCGTACTCG 242
      |||
QY      82 GINMESErSerLeuYsSerGIuAePTThrAlaLeuPheTYrCYeAlaArgHISArgSer 101
      |||
DB      243 CAAATGAGCAGTCTGAGGCTGAGACACATGCTGTATTATTGTGCCAAGACCTGTGTA 302
      |||
QY      102 G1YTYRPheserMeTAePTTYrTPGIYGINGIYThrSerValThrValSer 118
      |||
DB      303 AGTTACGCTGTTGATCATCTGGGCGCAAGGAGCACGCTCACCGTCTCC 353
      |||

RESULT 15
ABZ21159 standard; DNA, 366 BP.
XX
AC      ABZ21159;
XX
DT      28-MAR-2003 (first entry)
XX
DE      Variable region anti-bisphenol A antibody chain coding sequence #3.
XX
KW      Variable region; anti-bisphenol A; antibody; murine; heavy chain;
XX      light chain; gene; ds.
XX
OS      Mus sp.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..366
FT      FT      /*tag= a
FT      FT      /partial
FT      FT      /product= "Variable region anti-bisphenol A antibody
FT      FT      chain #3"
FT      FT      /note= "No start or stop codon given"
XX
PN      JP2002253259-A.
XX
PD      10-SEP-2002.
XX
PF      02-MAR-2001; 2001JP-00058673.
XX
PR      02-MAR-2001; 2001JP-00058673.
XX
PA      (BIO8-) BIO APPLIED SYSTEMS KK.
XX
DR      WPI, 2003-096537/09.
XX      P-PSDB; ABB98907.
XX
PT      Gene encoding anti-bisphenol A antibody, a recombinant protein and its
PT      preparation, a DNA, a vector, a transformant, preparation of a
PT      recombinant protein, a kit for determining bisphenol A.
XX
PS      Claim 1; Page 12; 19pp; Japanese.
XX
CC      The present invention relates to sequences for murine heavy chain
CC      variable region or light chain variable region of anti-bisphenol A
CC      antibody (ABZ21157-ABZ21164 and ABB98905-ABB98912). The sequences are

```

CC useful for the preparation of recombinant protein  
XX  
SQ Sequence 366 BP; 86 A; 88 C; 99 G; 93 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	7.05e-46	Length:	366
Score:	500.50	Matches:	100
Percent Similarity:	86.9%	Conservative:	6
Best Local Similarity:	82.0%	Mismatches:	13
Query Match:	81.1%	Indels:	3
DB:	8	Gaps:	2

US-10-635-908-6 (1-119) x ABZ21159 (1-366)

```
QY      1  AspValIlyLeuValGIuSerGIyGIyLeuValIlySerLeuIySerLeu 20
      1  GACGTGAAGTTCGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAGGCTCCGAAACTC 60
      21  SerCysAlaIaSerGIyPheThrPheSerAsnTyTYrMetSerTPValArgInThr 40
      61  TCAITGTCAAGCTCTGGAATTCATTTCAGAACTATTACATGCTTGGGTTCCGCAACT 120
      QY      41  ProGluLysArgLeuGIuLeuValAlaAlaIleAsnSerAspGIyGIyIleThrTYrTYr 60
      121  CCAAGAGAAGAGGCTGAGATTGTCGACGCAATTAATACCAATGGTGGTTTCACCTACTAT 180
      Db      61  LeuAspThrValIySGIyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTYr 80
      QY      81  LeuGlnMetSerSerLeuLysSerGIuAspThrAlaLeuPheTYrCysAlaArgHisArg 100
      Db      241  CTGCAATGACCACTCTGAAGTCTGAGGACACGGCCTTCTACTATTGTGCAAGACCGGAG 300
      QY      101  -----SerGIyTYrPheSer--MetAspTYrTrpGIyGlnGIyThrSerValThrVal 117
      Db      301  TTTGATACTTCTCACTAGAGCTGAGTTTGCTTACTGAGGCGCAAGGAGACTGTGTCACCTGTC 360
      QY      118  SerSer 119
      Db      361  TCTGCA 366
```

Search completed: June 3, 2006, 04:13:01  
Job time : 395.447 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Biocelebration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 04:13:15 ; Search time 2998.94 Seconds

(without alignments)  
3328.373 Million cell updates/sec

Title: US-10-635-908-6

Sequence: 1 DVKLVESSGGGLVKGSLKLT.....RSGYFMDYGGQTSVTYSS 119

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=rlh  
-Q=/abs/ABSWEB.spool/US10635908/runat\_02062006\_104216\_10273/app\_query.fasta\_1  
-DB=EST -QFMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS-bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h  
-USRR=US10635908.@CCN\_1\_17986.@runat\_02062006\_104216\_10273 -NCPU=6 -ICPU=3  
-NO\_WAMP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMOUT=120  
-WAMP TIMOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.\*  
1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_est7.\*  
7: gb\_est8.\*  
8: gb\_est9.\*  
9: gb\_est10.\*  
10: gb\_est11.\*  
11: gb\_gss1.\*  
12: gb\_gss2.\*  
13: gb\_gss3.\*  
14: gb\_gss4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495.5	80.3	861	2	BI455668
2	495	80.2	603	3	BQ266309
3	494	80.1	650	7	BF579001
4	482	78.1	774	7	BF581450

5	478.5	77.6	837	2	BQ66335	BQ66335	602832843
6	468.5	75.9	987	7	BF577496	BF577496	602092343
7	466	75.5	689	7	BF579926	BF579926	602095194
8	465.5	75.4	823	1	AA170256	AA170256	m87910.r
9	456	73.9	662	7	BF163874	BF163874	601772386
10	455	73.7	1012	7	BF142302	BF142302	601791844
11	454.5	73.7	562	9	DA975437	DA975437	DA975437
12	453.5	73.5	583	9	DA976755	DA976755	DA976755
13	453.5	73.5	554	9	DA972115	DA972115	DA972115
14	453.5	73.5	667	4	BY750520	BY750520	BY750520
15	453.5	73.5	1565	6	AK156019	AK156019	Mus muscu
16	452.5	73.3	552	9	DA982966	DA982966	DA982966
17	451	73.1	901	3	BUS23851	BUS23851	AGENCOURT
18	450.5	73.0	562	9	DA980210	DA980210	DA980210
19	450	72.9	913	7	BF162056	BF162056	BF162056
20	449	72.8	557	9	DA972534	DA972534	DA972534
21	449	72.8	559	9	DA979611	DA979611	DA979611
22	449	72.8	560	9	DA987096	DA987096	DA987096
23	449	72.8	573	9	DA980582	DA980582	DA980582
24	448.5	72.7	777	5	CK476776	CK476776	AGENCOURT
25	447.5	72.5	469	1	AI645111	AI645111	m87910.y
26	447	72.4	498	9	DA971158	DA971158	DA971158
27	446.5	72.4	546	9	DA947087	DA947087	DA947087
28	446	72.3	969	7	BF579260	BF579260	602093431
29	445.5	72.2	504	9	DA977056	DA977056	DA977056
30	445.5	72.2	580	9	DA988280	DA988280	DA988280
31	445.5	72.2	1586	6	BC018461	BC018461	Mus muscu
32	445.5	72.1	550	9	DA976042	DA976042	DA976042
33	445	72.1	579	9	DA974187	DA974187	DA974187
34	444.5	72.0	593	9	DB190243	DB190243	DB190243
35	444	72.0	550	9	DA975094	DA975094	DA975094
36	444	72.0	875	3	BQ706723	BQ706723	AGENCOURT
37	444	72.0	968	3	BQ706746	BQ706746	AGENCOURT
38	443	71.8	545	9	DB102282	DB102282	DB102282
39	443	71.8	561	9	DA983749	DA983749	DA983749
40	442.5	71.7	572	9	DA954615	DA954615	DA954615
41	442.5	71.7	572	9	DA981934	DA981934	DA981934
42	442	71.6	578	9	DA820045	DA820045	DA820045
43	442	71.6	908	7	BF161883	BF161883	601766819
44	441.5	71.6	515	4	CA571547	CA571547	K0521E06-
45	441.5	71.6	542	9	DA971342	DA971342	DA971342

#### ALIGNMENTS

RESULT 1  
BI455668  
LOCUS 861 bp mRNA linear EST 21-AUG-2001  
DEFINITION 603173862F1 NCT\_CGAP\_Mams Mus musculus cDNA clone IMAGE:5253279 5',  
mRNA sequence.  
ACCESSION BI455668  
VERSION BI455668.1 GI:15246324  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 861)  
NTH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
Plate: LHAM1639 row: 1 column: 16  
High quality sequence stop: 780.

FEATURES  
source  
Location/Qualifiers  
1. 861  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="mix FVB/N, C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5253279"  
/issue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/clone\_11b="NCI CGAP Mam5"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt; Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

ORIGIN  
Alignment Scores:  
Pred. No.: 2.5e-55 Length: 861  
Score: 495.50 Matches: 97  
Percent Similarity: 89.9% Conservative: 10  
Best Local Similarity: 81.5% Mismatches: 11  
Query Match: 80.3% Indels: 1  
DB: 2 Gaps: 1

US-10-635-908-6 (1-119) x B1455668 (1-861)

QY 1 AapvallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuValLeu 20  
::: 128 GAAGTGAAGCTGGTGGAGCTGGGGAGGCTTAGTCAGCCTGGAGAGGCTCCCGAAATC 187  
QY 21 SerCyAlAlASerGlyPheThrPheSerAenTyTyMetSerTrpValArgGlnTr 40  
DB 188 TCTGTGCAACCTCTGGATTCATTACGTATTAATGAGGTTGCCAGACT 247  
QY 41 ProGluLyArgLeuGluLeuValAlaAlaIleAenSerAapGlyGlyIleThrTyTy 60  
DB 248 CAGAGAAAGGCTGGAGTGGCTGCATCATTAGTAATGGTGGTGGTGCACCTATTAT 307  
QY 61 LeuAapThrVallyGlyArgPheThrIleSerArgAapAaAlaAlaAenThrLeuTy 80  
DB 308 CAGACACTGTAAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 367  
QY 81 LeuGlnMetSerSerLeuTySerGluAapThrAlaLeuPheTyTyCyAlaArgHisArg 100  
DB 368 CTGCACAATAGACGCTGTGAAGTCTGAGACACAGCCATGATTATTCGTCCAAAGA--ACT 424  
QY 101 SerGlyTyPheSerMetAapTyTyTrpGlyGlnGlyThrSerValThrValSerSer 119  
DB 425 AACTGTAATGCTATGCTATGCACTACTGGGGTCAAGAACTCACTCACTCTCTCTCA 481

RESULT 2  
BQ266309 603 bp mRNA linear EST 07-MAY-2002  
LOCUS BQ266309.1 NCI CGAP Mam5 Mus musculus cDNA clone IMAGE:2865417  
DEFINITION 5' mRNA sequence.  
ACCESSION BQ266309  
VERSION BQ266309.1 GI:20491374  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: Lothar Hennighausen/Robin Humphreys

CDNA Library Preparation: Life Technologies  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NIH)  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov  
MG1:1046189  
Plate: L1AM7069 row: F column: 10  
Seq primer: M13Rpl reverse primer (ABI).  
Location/Qualifiers  
1. 603  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="mix FVB/N, C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:2865417"  
/issue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/clone\_11b="NCI CGAP Mam5"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt; Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.75e-55 Length: 603  
Score: 495.00 Matches: 96  
Percent Similarity: 91.6% Conservative: 13  
Best Local Similarity: 80.7% Mismatches: 8  
Query Match: 80.2% Indels: 2  
DB: 3 Gaps: 1

US-10-635-908-6 (1-119) x BQ266309 (1-603)

QY 1 AapvallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuValLeu 20  
::: 132 GAGGTGCACCTGGTGAAGCTGGGGAGGCTTAGGAAGCTGGTGGTCCCGAAATC 191  
QY 21 SerCyAlAlASerGlyPheThrPheSerAenTyTyMetSerTrpValArgGlnTr 40  
DB 192 TCTGTGCAACCTCTGGATTCATTACGTATTAATGAGGTTGCCAGACT 251  
QY 41 ProGluLyArgLeuGluLeuValAlaAlaIleAenSerAapGlyGlyIleThrTyTy 60  
DB 252 CCGAAGAAAGGCTGGAGTGGCTGCAGCATTAATTAATGAGGTTGCCAGACT 311  
QY 61 LeuAapThrVallyGlyArgPheThrIleSerArgAapAaAlaAlaAenThrLeuTy 80  
DB 312 CAGACACTGTAAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 371  
QY 81 LeuGlnMetSerSerLeuTySerGluAapThrAlaLeuPheTyTyCyAlaArgHisArg 100  
DB 372 CTGCACAATAGACGCTGTGAAGTCTGAGACACAGCCCTGATTATTCAGTTCAACATGCT 421  
QY 101 SerGlyTyPheSerMetAapTyTyTrpGlyGlnGlyThrSerValThrValSerSer 119  
DB 432 AACTTCTACTTT-----GACTACTGGGGCCAAGCACCACTCTCACTCTCTCA 482

RESULT 3  
BF579001 650 bp mRNA linear EST 12-DEC-2000  
LOCUS BF579001 602096117F1 NCI CGAP Co24 Mus musculus cDNA clone IMAGE:4215844 5'  
DEFINITION mRNA sequence.  
ACCESSION BF579001  
VERSION BF579001.1 GI:11652713  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia: Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
1 (bases 1 to 650)  
NHL-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LLM9792 row: b column: 05  
High quality sequence stop: 649.  
Location/Qualifiers

## FEATURES

source

1. 650  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4215844"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

## Alignment Scores:

Pred. No.:	2,666-55	Length:	650
Score:	494.00	Matches:	102
Percent Similarity:	90.0%	Conservative:	6
Best Local Similarity:	85.0%	Mismatches:	7
Query Match:	80.1%	Indels:	5
DB:	7	Gaps:	1

US-10-635-908-6 (1-119) x BF579001 (1-650)

```
QY 1 AspValLyLeuValGluSerGlyGlyLeuValLyLeuGlyGlySerLeuLyLeu 20
   :::::::::::
Db 128 GAGGTGACGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGAGAGGTCCTGAAACTC 187

QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyRTyrMetSerTPValArgGlnThr 40
   :::::::::::
Db 188 TCCGTGCACGCTCTGATTCACTTCAGTAACATGAGCATGCTTGGGTCGCGCAACT 247

QY 41 ProGluLySarGluLeuValAlaAlaLeuSerAspGlyGlyLeuThrTyTy 60
   :::::::::::
Db 248 CCGAGAGAGAGGCTGGAGTGGTGCAGCCATTAAATGATGATGTAACACTTACTAT 307

QY 61 LeuAspThrValLyGlyArgPheThrIleSerArgAspAsnAlaLyAsnThrLeuTy 80
   :::::::::::
Db 308 CCAGACACTGTGAAGGGCCGATTCACCATCTCCAGAGCAATGCGCAAGAACACCTGTAT 367

QY 81 LeuGlnMetSerSerLeuLySerGluAspThrAlaLeuPheTyTyCys-AlaArgHisAr 100
   :::::::::::
Db 368 CTGACAGATGAGCACTGAGGCTGAGAGACACACCTTGATTACTGTTGCAAGACAT- 425

QY 100 gSerGlyTyRPhSerMetAspTyRTyrGlyGlnGlyThySerValThrValSerSer 119
   :::::::::::
Db 426 -----CTGACTATGACTACTGGGGTCAAGAGAACCTCAGTCAACGCTCTCTCA 473
```

## RESULT 4

BF581450 774 bp mRNA linear EST 12-DEC-2000  
LOCUS 602100853p1 NCI\_CGAP\_C024 Mus musculus cDNA clone IMAGE:4224109 5',  
DEFINITION mRNA sequence.  
ACCESSION BF581450  
VERSION BF581450.1 GI:11655162

KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Mammalia: Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
1 (bases 1 to 774)  
NHL-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LLM9813 row: j column: 14  
High quality sequence stop: 675.  
Location/Qualifiers

## FEATURES

source

1. 774  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4224109"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

## Alignment Scores:

Pred. No.:	1,396-53	Length:	774
Score:	482.00	Matches:	96
Percent Similarity:	84.8%	Conservative:	10
Best Local Similarity:	76.8%	Mismatches:	13
Query Match:	78.1%	Indels:	6
DB:	7	Gaps:	1

US-10-635-908-6 (1-119) x BF581450 (1-774)

```
QY 1 AspValLyLeuValGluSerGlyGlyLeuValLyLeuGlyGlySerLeuLyLeu 20
   :::::::::::
Db 118 GAGGTGACGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGAGAGGTCCTGAAACTC 177

QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyRTyrMetSerTPValArgGlnThr 40
   :::::::::::
Db 178 TCCGTGCACGCTCTGATTCACTTCAGTAACATGAGCATGCTTGGGTCGCGCAACT 237

QY 41 ProGluLySarGluLeuValAlaAlaLeuSerAspGlyGlyLeuThrTyTy 60
   :::::::::::
Db 238 CCGAGAGAGAGGCTGGAGTGGTGCAGCCATTAAATGATGATGTAACACTTACTAT 297

QY 61 LeuAspThrValLyGlyArgPheThrIleSerArgAspAsnAlaLyAsnThrLeuTy 80
   :::::::::::
Db 298 CTAGACCTGTGAAGGGCCGATTCACCATCTCCAGAGCAATGCGCAAGAACACCTGTAT 357

QY 81 LeuGlnMetSerSerLeuLySerGluAspThrAlaLeuPheTyTyCysAlaArgHisArg 100
   :::::::::::
Db 358 CTGCAATGACAGTCTGAGGCTGAGAGACACACCTTGATTACTGTTGCAAGACATGG 417

QY 101 -----SerGlyTyRPhSerMetAspTyRTyrGlyGlnGlyThySerValThrValSerSer 114
   :::::::::::
Db 418 GATATATATGCTACTATTAAGAGAGTACTTGTGACTTATGGGCGCAAGCACCACT 477

QY 115 ValThrValSerSer 119
   :::::::::::
Db 478 CTCACAGTCTCTCTCA 492
```

RESULT 5  
BG966355 837 bp mRNA linear EST 12-JUN-2001  
LOCUS 602832843f1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4987379 5',  
DEFINITION mRNA sequence.  
ACCESSION BG966355  
VERSION BG966355.1 GI:14353392  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov.  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10998 row: e column: 12  
High quality sequence stop: 692.  
Location/Qualifiers  
1..837  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4987379"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_1ib="NCI CGAP Co24"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: NCI;  
Site\_2: Sall; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
ORIGIN  
Alignment Scores:  
Pred. No.: 4,59e-53 Length: 837  
Score: 478.50 Matches: 96  
Percent Similarity: 86.7% Conservative: 8  
Best Local Similarity: 80.0% Mismatches: 15  
Query Match: 77.6% Indels: 1  
DB: 2 Gaps: 1  
US-10-635-908-6 (1-119) x BG966355 (1-837)  
QY 1 AspValIyLeuValIguSerIygiYlLeuValIyLeuIygiYserIeulysLeu 20  
Db 135 GAAGTATGCTGCTGGAGTCTGGGGAGGCTTAGTAAGCCTGAGAGGCTCCGAAATC 194  
QY 21 SerCyAlAlAlaSerIyPheThrPheSerAntyTyTyMetSerTryValArgIntnr 40  
Db 195 TCCTGTGACAGCCTCGATTCACCTTCAGTAGCTATACCATGCTTGGGTTCCGACAGCT 254  
QY 41 ProGluIyArGleuGluIuLeuValAlAlaIleAsnSerAspIygiYIleThrTyTy 60  
Db 255 CCGGCGAAGAGGCTGAGGAGGTCGCAACCATTAAGTGCTGTGATTAACACTACTAT 314  
QY 61 LeuAspThrValIygiYArGPhetnriIleSerArxAspAsnAlaIysAsnThrLeuTy 80  
Db 315 CCGAAGAAATATGAGGCGCATTCACCATTCAGAGACATCCAGAAACCCCTGTAC 374  
QY 81 LeuGImetSerSerIeulysSerIyAspThrAlaLeuPheTyCyAlArGHIaTy 100  
Db 375 CTCGAATATGAGCTGAGAGCTGAGAGACCGGCTGTATTAATCTGTGACAGACGGGTT 434

QY 101 SerGly---TyrPheSerMetAspTyTyTrpGlyGlnGlyThsSerValThrValSerSer 119  
Db 435 TATGTACTCTTATGATGATGAGTCTGGGGTCAAGAACTCATGTCACCGTCTCTCA 494  
RESULT 6  
BF577496 987 bp mRNA linear EST 12-DEC-2000  
LOCUS 602092343f1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4206707 5',  
DEFINITION mRNA sequence.  
ACCESSION BF577496  
VERSION BF577496.1 GI:11651208  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov.  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9768 row: e column: 12  
High quality sequence start: 3  
High quality sequence stop: 699.  
Location/Qualifiers  
1..987  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4206707"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_1ib="NCI CGAP Co24"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: NCI;  
Site\_2: Sall; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
ORIGIN  
Alignment Scores:  
Pred. No.: 1,28e-51 Length: 987  
Score: 468.50 Matches: 93  
Percent Similarity: 85.0% Conservative: 9  
Best Local Similarity: 77.5% Mismatches: 17  
Query Match: 75.9% Indels: 1  
DB: 7 Gaps: 1  
US-10-635-908-6 (1-119) x BF577496 (1-987)  
QY 1 AspValIyLeuValIguSerIygiYlLeuValIyLeuIygiYserIeulysLeu 20  
Db 107 GATGTACACTGCTGAGTCTGGGGAGGCTTAGTACACCTGAGAGGCTCCGAAATC 166  
QY 21 SerCyAlAlAlaSerIyPheThrPheSerAntyTyTyMetSerTryValArgIntnr 40  
Db 167 TCCTGTGACAGCCTCGATTCACCTTCAGTAGCTATGAATGACATGGTTCGTCAAGCT 226  
QY 41 ProGluIyArGleuGluIuLeuValAlAlaIleAsnSerAspIygiYIleThrTyTy 60  
Db 227 CCGAAGAAAGGCTGAGGAGGTCGCAATATATTGATAGAGAGTGTACCATCTACTAT 286  
QY 61 LeuAspThrValIygiYArGPhetnriIleSerArxAspAsnAlaIysAsnThrLeuTy 80

Db	287	CGAGACACAGGAGGAGGCCGACCTTACCATCTCCAGAGACATGGCAAGAACACCCCTGTC	346
Qy	81	LeuGlnMetSerSerLeuLeuSerSerGluAspThrAlaLeuPheTyrCysAlaIleHisArg	100
Db	347	CTGCAATATGACCATCTTAAAGCTCTGAGAGACAGGCCCATGTTATCTGTCGAAGACGCTAT	406
Qy	101	SerGly---TyrPheSerMetAspTyrTThrGlyGlnGlyThrSerValThrValSerSer	119
Db	407	AGTAAACCATTAATTGTCATGACTACTAGGAGGAGTCAAGAACCTCAGTCACGCTCTCTCA	466
RESULT 7			
LOCUS	BF579926		
DEFINITION	BF579926	689 bp	mRNA linear EST 12-DEC-2000
ACCESSION	602095194F1	NCI_CGAP_Co24	Mus musculus cDNA clone IMAGE:4209551 5',
VERSION	BF579926		mRNA sequence.
KEYWORDS	BF579926.1	GI:11653638	
SOURCE	EST.		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Mus musculus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
JOURNAL	Sciurionathi; Murioidea; Muridae; Murinae; Mus.		
COMMENT	1 (bases 1 to 689)		
	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>		
	Tissue Procurement: Jeffrey E. Green, M.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>		
	Plate: LLM9775	row: k	column: 24
FEATURES	High quality sequence	stop: 685.	
Source	Location/Qualifiers		
	1..689		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/strain="FVB/N"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:4209551"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/clone_11b="NCI_CGAP_Co24"		
	/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;		
	Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.		
	Average insert size 1.6 kb. Constructed by life		
	Technologies. Note: this is a NCI_CGAP Library."		
ORIGIN			
Alignment Scores:			
Pred. No.:	1..666-51	Length:	669
Score:	466.00	Matches:	96
Percent Similarity:	88.3%	Conservative:	10
Best Local Similarity:	80.0%	Mismatches:	9
Query Match:	75.5%	Indels:	5
DB:	7	Gaps:	2
US-10-635-908-6 (1-119) x BF579926 (1-689)			
Qy	1	AspValValLeuValGluSerGlyGlyValLeuValValLeuGlyGlySerLeuValLeu	20
Db	131	GAGGTCCACCTGGTGAAGTCTGGGGGAGGCTTAGTAAGACCTGGAGGGTCCCTGGAAGTTC	190
Qy	21	SerCysAlaIleAserGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr	40
Db	191	TCTGTGCGAGCCCTCTGGATTCACTTTCAGTAATAGCCATGCTTGGGTGGCCAGAGT	250
Qy	41	ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr	60

Dn		251	CCGGAAGAAGCGCTGGAGTGGGTCCGACGCATTAAATGTAATGGTGTAATCACTACT	310
Oy		61	LeuasPthrValIysGIaRgphethrIIeseraTaSPasnaAlalysanThrlentYr	80
Dn		311	TGACAACATAAGTAAGGCGCATTCACCACTCTTAGAGAACATGCCAAGCACCCCTGTAT	370
Oy		81	LeuGlImetSerterleumIysserGIuaapThAla-LeupeTyfCySaAlakhtIsar	100
Dn		371	CTGCCAATATGACGCTGTGAGCTGTGAGACACGCCCTTTATATATATGTGTGA-----AG	424
Oy		100	gSergLyTYPhSeSerMetAspyTrtTpplngInglYThrSerValThrValserSer	119
Dn		425	AGGGGGGTACTTC-----CATCTCTGGGGCGCAGGAGCCGGCGTACCCTCTCTCA	476
RESULT 8				
LOCUS	AA170256			
DEFINITION	mus musculus muscle 3nbms Mus musculus cDNA clone IMAGE:618594			
KEYWORDS	EST.			
VERSION	AA170256			
ORGANISM	Mus musculus (house mouse)			
REFERENCE	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gaisel,S., Kucaba,T., Lacy,W., Le,M., Martin,J., Morris,M., Schellemberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.			
JOURNAL COMMENT	The WashU-HMI Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mousesewatson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium ( <a href="mailto:info@image.lnl.gov">info@image.lnl.gov</a> ) for further information. MG1:379418 Putative full length read vector to vector length is 867 Seq primer: -28M13 revz from Amersham High quality sequence stop: 492. location/Qualifiers 1..823 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:618594" /sex="male" /tissue-type="Spleen" /dev_stage="4 weeks" /lab_host="DH10B" /clone_1kb="Soares mouse 3NBMS" /note="Vector: pUT3D-PacI; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15' TGTTACCAATCTGAAGTGGAGCGCGCCGCTGTTTTTTTTTTTTTTTTTTTTTTTTT 3'1'; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pUT3D vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."			

## ORIGIN

## Alignment Scores:

Pred. No.:	2,496-51	Length:	823
Score:	465.50	Matches:	93
Percent Similarity:	84.4%	Conservative:	10
Best Local Similarity:	76.2%	Mismatches:	16
Query Match:	75.4%	Indels:	3
DB:	1	Gaps:	1

US-10-635-908-6 (1-119) x AA170256 (1-823)

```
QY 1 AAPPVLLYSLVLEUVALGLUSERGLYGLYGLYSLVLEUVALYGLYSERLEUYSLEU 20
DB 118 GAGGTGAGAGCTGTGAGGTCTGGAGAGCTTAGTGAAGCTGGAGAGGCTCCCTGAAGACTC 177
QY 21 SERCYAALALASERGLYPHERPHERPHERSERASNTYTYMETSETRYVALARGINTHR 40
DB 178 TCTGTGACGCTTGGATTCACTTTCAGTACTATGCCATGTCTGGGTGGCCAGACT 237
QY 41 PROGLULYARGLUENGLULEUVALALALALEASERASPGLYGLYILETHRYTYR 60
DB 238 CCAGAGAAAGAGCTGAGAGGTGGTGCATACATTAGTAGTGTGATTACATCTACTAT 297
QY 61 LEUAPTHVALYGLYARPHETHRILESERARASAPNALALYASANTHRILEUTYR 80
DB 298 GCAGACACTGTGAGAGGCCGATTCACCATCTCCAGACAAATGCCAGAACACCTGTAC 357
QY 81 LEUINMETSERSERLEUYSERGLYUAPTHRALALEUPHETRYCYAALAAARG----- 98
DB 358 CTGCAAAATGAGAGCTGAGAGTCTGAGAGACAGAGCATATTAATCTGACAGAGATGCC 417
QY 99 ---HISARGSERGLYTYRPHESERMETAPRYTTPGLYGLINGLYTHSERVALTHRYVAL 117
DB 418 CTCTAGTACTGTGGTCTACTACTTGTGACTACTGAGGCAAGGACCACTCTCACAGTTC 477
QY 118 SERSER 119
DB 478 TCTCTCA 483
```

RESULT 9  
BFL63874 662 bp mRNA linear EST 30-OCT-2000  
LOCUS BFL63874  
DEFINITION mRNA sequence.  
ACCESSION BFL63874  
VERSION BFL63874.1 GI:11044152  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
TITLE Sciurognathi; Muridae; Murinae; Mus.  
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

FEATURES  
source  
1..662  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="Czech II"  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LHAM9204 row: 1 column: 21  
High quality sequence stop: 658.  
Location/Qualifiers

## ORIGIN

```
/db_xref="taxon:10090"  
/clone="IMAGE:3991460"  
/tissue_type="spontaneous tumor, metastatic to mammary.  
Stem cell origin."  
/lab_host="DH10B"  
/clone_lib="NCI CGAP Lu29"  
/note="Organ: Lung; Vector: pCMV-SPORT6; Site: 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"
```

## Alignment Scores:

Pred. No.:	3,446-50	Length:	662
Score:	456.00	Matches:	96
Percent Similarity:	86.8%	Conservative:	9
Best Local Similarity:	79.3%	Mismatches:	12
Query Match:	73.9%	Indels:	4
DB:	7	Gaps:	3

US-10-635-908-6 (1-119) x BFL63874 (1-662)

```
QY 1 AAPPVLLYSLVLEUVALGLUSERGLYGLYGLYSLVLEUVALYGLYSERLEUYSLEU 20
DB 123 GAGGTGAGAGCTGTGAGGTCTGGAGAGCTTAGTGAAGCTGGAGAGGCTCCCTGAAGACTC 182
QY 21 SERCYAALALASERGLYPHERPHERPHERSERASNTYTYMETSETRYVALARGINTHR 40
DB 183 TCTGTGACGCTTGGATTCACTTTCAGTACTATGCCATGTCTGGGTGGCCAGACT 242
QY 41 PROGLULYARGLUENGLULEUVALALALALEASERASPGLYGLYILETHRYTYR 60
DB 243 CCAGAGAAAGAGCTGAGAGGTGGTGCATACATTAGTAGTGTGATTACATCTACTAT 299
QY 61 LEUAPTHVALYGLYARPHETHRILESERARASAPNALALYASANTHRILEUTYR 80
DB 300 CCAGACAGTGTGAGAGGTGATTCACCATCTCCAGACAAATGCCAGAACACCTGTAC 359
QY 81 LEUINMETSERSERLEUYSERGLYUAPTHRALALEUPHETRYCYAALAAARGHISARG 100
DB 360 CTCCAAATGAGAGCTGAGAGTCTGAGAGACAGAGCATATTAATCTGACAGAGA---CGT 416
QY 101 SERGLYTYRPHESER-----METAPRYTTPGLYGLINGLYTHSERVALTHRYVALSER 118
DB 417 GGTGTACTTAGGAGATGATCTTCATCTGCTGTGGGCGCAGGAGACACAGGTCACTCC 476
QY 119 SER 119
DB 477 TCA 479
```

RESULT 10  
BFL42302 1012 bp mRNA linear EST 24-OCT-2000  
LOCUS BFL42302  
DEFINITION mRNA sequence.  
ACCESSION BFL42302  
VERSION BFL42302.1 GI:10981252  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
TITLE Sciurognathi; Muridae; Murinae; Mus.  
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

FEATURES  
source  
1..662  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="Czech II"  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LHAM9279 row: h column: 12  
High quality sequence stop: 711.  
Location/Qualifiers

## FEATURES

source

1.1012  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="Czech 11"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4022459"  
/issue\_type="tumor, metastatic to mammary"  
/lab\_host="DH10B"  
/clone\_1ib="NCI-CGAP Lu30"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; transgenic model MMT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies.  
Investigator providing samples: Gilbert Smith, NIH"

## ORIGIN

## Alignment Scores:

Pred. No.: 8,586-50 Length: 1012  
Score: 455.00 Matches: 91  
Percent Similarity: 84.0% Conservative: 9  
Best Local Similarity: 76.5% Mismatches: 17  
Query Match: 73.7% Indels: 2  
DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x BFL42302 (1-1012)

QY 1 AspvAllyleuValGluSerGlyGlyLeuValylsLeuGlySerLeuValLeu 20  
101 GAGGTGAGCTGGGAGCTGGGGAGGCTTGTGAGAGCTGGAGGCTCCGAAACTC 160  
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrtMetSerTPValArgInThr 40  
161 TCCTGTGACCTCTGTGATTCACCTTCAGTGACATGGAATGCACTGGTTCGACAGCT 220  
QY 41 ProGluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyIleThrTyrt 60  
221 CCAGAGAAAGGGCTGGAGTGGTGCATACATAGTGGCAGTACATCCTACTAT 280  
QY 61 LeuAspThrValylsGlyArgPheThrIleSerArgAspAlaValAsnThrLeuTy 80  
281 GCAGACACAGTGAAGGGCCGATTCACATCCAGAGCAATGCAAGAACACCTGTC 340  
QY 81 LeuGlnMetSerSerLeuLysSerGlyAspThrAlaLeuPheTyrtCyAlaArgHisArg 100  
341 CTGCAATATGACCATCTAAGGTCTGAGACACGCCCATGTATCTGTGCA-----AGC 394  
QY 101 SerGlyTyrtPheSerMetAspTyrtTyrGlyGlnGlyThrSerValThrValSerSer 119  
395 CCAAGTACTCTCCCTATGACTACTGAGGCTCAAGAACTCAGTCACCGTCTCTCA 451  
RESULT 11  
DA975437 562 bp mRNA linear EST 13-NOV-2005  
LOCUS DA975437 SYN02 Homo sapiens cDNA clone SYN02005900 5', mRNA  
DEFINITION sequence.  
ACCESSION DA975437 GI:82346288  
VERSION DA975437.1 GI:82346288  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 562)  
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,  
Yamashita,R., Yamamoto,J., Sekine,M., Teuriltan,K., Wakaguri,H.,  
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kishida,N.,

## TITLE

JOURNAL  
PUBMED  
COMMENT

Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,  
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi,Fuji,A.,  
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T., and Sugano,S.  
Diversification of Transcriptional Modulation: Large-scale  
Identification and Characterization of Putative Alternative  
Promoters of Human Genes  
Genome Res. 16 (1), 55-65 (2006)  
16344560  
Contact: Takao Isogai  
FLJ Project (HRI Team)  
Helix Research Institute  
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: flj-cdna@nifty.com  
NEDO human cDNA project (New Energy and Industrial Technology  
Developmental Organization, Japan); cDNA library construction;  
Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,  
Research Association for Biotechnology (RAB) and Biotechnology  
Center, National Institute of Technology and Evaluation; 3'-end one  
pass sequencing; RAB.  
Location/Qualifiers

## FEATURES

source

1.562  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="SYNOV2005900"  
/issue\_type="synovial membrane tissue from rheumatoid  
arthritis"  
/clone\_1ib="SYNOV2"  
/note="Vector: pME18SFU3"

## ORIGIN

## Alignment Scores:

Pred. No.: 4,336-50 Length: 562  
Score: 454.50 Matches: 88  
Percent Similarity: 86.4% Conservative: 14  
Best Local Similarity: 74.6% Mismatches: 15  
Query Match: 73.7% Indels: 1  
DB: 9 Gaps: 1

US-10-635-908-6 (1-119) x DA975437 (1-562)

QY 2 ValylsLeuValGluSerGlyGlyLeuValylsLeuGlySerLeuValLeuSer 21  
142 GTGAGCTGGTGGAGTCTGGGGAGGCTGTGATCAGGCTGGAGGCTCTGAGACTCTCC 201  
QY 22 CyAlaAlaSerGlyPheThrPheSerAsnTyrtMetSerTPValArgInThrPro 41  
202 TGTGACACCTCTGTGATTCACCTTCAGTACTACTAGTGAAGTGAATCCGACAGCTCA 261  
QY 42 GluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyIleThrTyrt 61  
262 GCGAAGGCGCTGAGTGGTTCATACATTAAGTACTGATAGACATATACAGCA 321  
QY 62 AspThrValylsGlyArgPheThrIleSerArgAspAlaValAsnThrLeuTy 81  
322 GACTCTGGAAGGGCCGATTCACCATCTCCAGGAGCAACGCAAGCACTCATCTG 381  
QY 82 GlnMetSerSerLeuLysSerGlyAspThrAlaLeuPheTyrtCyAlaArgHisArgSer 101  
382 CAAATGAACAGCCCTGAAGCCGAGAGACACGCCCTGTATTACTGTGACAGCAAGAGAT 441  
QY 102 GlyTyrtPheSerMetAspTyrtTyrGlyGlnGlyThrSerValThrValSerSer 119  
442 GCGTAT---AACTTGACTACTGGGCGAGGAACCTGTGACCGTCTCTCA 492  
RESULT 12  
DA976755 553 bp mRNA linear EST 13-NOV-2005  
LOCUS DA976755 SYN02 Homo sapiens cDNA clone SYN02005400 5', mRNA  
DEFINITION sequence.  
ACCESSION DA976755

```

VERSION      DA976755.1 GI:82369686
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Mammalia; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
              Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
              Homnidae; Homo.
REFERENCE    1 (bases 1 to 553)
AUTHORS      Kimura,K., Wakamatsu,A., Suzuki,Y., Oca,T., Nishikawa,T.,
              Yamashita,R., Yamamoto,J., Sekine,M., Teuricani,K., Wakaquri,H.,
              Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
              Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Magetsuma,M.,
              Murakawa,K., Ishida,S., Ishibashi,T., Takahashi,Fuji,A.,
              Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
              Diversification of Transcriptional Modulation: Large-scale
              Identification and Characterization of Putative Alternative
              Promoters of Human Genes
JOURNAL      Genome Res. 16 (1), 55-65 (2006)
PUBMED
COMMENT      Contact: Takao Isogai
              PIJ Project (HRI Team)
              Helix Research Institute
              2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
              Tel: 81-438-52-3975
              Fax: 81-438-52-3986
              Email: filj-cdna@nifty.com
              NEDO human cDNA project (New Energy and Industrial Technology
              Developmental Organization, Japan); cDNA library construction:
              Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
              Research Association for Biotechnology (RAB) and Biotechnology
              Center, National Institute of Technology and Evaluation; 3'-end one
              pass sequencing: RAB.
FEATURES
  source
    1..553
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="SYNOV2007540"
        /issue_type="synovial membrane tissue from rheumatoid
        arthritis"
        /clone_lib="SYNOV2"
        /note="Vector: PME18SFL3"
ORIGIN
Alignment Scores:
Pred. No.:      5..766-50      Length:      553
Score:          453.50      Matches:      88
Percent Similarity: 83.7%      Conservative: 15
Best Local Similarity: 71.5%      Mismatches: 15
Query Match:    73.5%      Indels:      5
DB:             9      Gaps:      1
US-10-635-908-6 (1-119) x DA976755 (1-553)
QY      2 valvsleuvalgluserglyglylyleuvallyleuuglyglyserleuylsleuser 21
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      141 gtgcacctggtgagctgggggagagcttgctcaacctggagagctccctgagacctctcc 200
QY      22 cysalalaserglyphethrpheserasytyrtyrmetsertrypvalargintnprco 41
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      201 tctgcagcctctgattcacttcactgactactactagactgactgactcccgagcgtcca 260
QY      42 gtlvysargleuugluuvalalalalalaasnsersaspglyglyliethrtyrtyrleu 61
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      261 gggaagagggctgagagggcttcattacattagtagtagtgaatcacatatactactagcca 320
QY      62 aspthvallyaglyvarghethrtrilesersargasphalalaysanthrtrileu 81
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      321 gactctgtgaaaggccgattccaccatctccaggagacacggccaggaactcactgtacttg 380
QY      82 glmetserseleuysersergluaspthalaleuphetyrcysalalarghtsargser 101
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      381 caaatgaaacgcttgagagccgagacacggccgctgattactctgagagactcaccgggt 440

```

```

QY      102 gty-----tyrphesermetaptyrtyrpglynglythrservalthr 116
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      441 ggtcactcttactactactactagtagagctctggggccaaaggagccacgctcacc 500
QY      117 valserser 119
      |||:::|||||
DB      501 gttctctcca 509
RESULT 13
DA972115      584 bp mRNA linear EST 11-NOV-2005
LOCUS      DA972115
DEFINITION      DA972115 SYN0V2 Homo sapiens cDNA clone SYN0V2001766 5', mRNA
sequence.
ACCESSION      DA972115 GI:82114937
VERSION      DA972115.1
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
              Homnidae; Homo.
REFERENCE    1 (bases 1 to 584)
AUTHORS      Kimura,K., Wakamatsu,A., Suzuki,Y., Oca,T., Nishikawa,T.,
              Yamashita,R., Yamamoto,J., Sekine,M., Teuricani,K., Wakaquri,H.,
              Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
              Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Magetsuma,M.,
              Murakawa,K., Ishida,S., Ishibashi,T., Takahashi,Fuji,A.,
              Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
              Diversification of Transcriptional Modulation: Large-scale
              Identification and Characterization of Putative Alternative
              Promoters of Human Genes
JOURNAL      Genome Res. 16 (1), 55-65 (2006)
PUBMED
COMMENT      Contact: Takao Isogai
              PIJ Project (HRI Team)
              Helix Research Institute
              2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
              Tel: 81-438-52-3975
              Fax: 81-438-52-3986
              Email: filj-cdna@nifty.com
              NEDO human cDNA project (New Energy and Industrial Technology
              Developmental Organization, Japan); cDNA library construction:
              Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
              Research Association for Biotechnology (RAB) and Biotechnology
              Center, National Institute of Technology and Evaluation; 3'-end one
              pass sequencing: RAB.
FEATURES
  source
    1..584
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="SYNOV2001766"
        /issue_type="synovial membrane tissue from rheumatoid
        arthritis"
        /clone_lib="SYNOV2"
        /note="Vector: PME18SFL3"
ORIGIN
Alignment Scores:
Pred. No.:      6..236-50      Length:      584
Score:          453.50      Matches:      87
Percent Similarity: 83.7%      Conservative: 16
Best Local Similarity: 70.7%      Mismatches: 15
Query Match:    73.5%      Indels:      5
DB:             9      Gaps:      1
US-10-635-908-6 (1-119) x DA972115 (1-584)
QY      2 valvsleuvalgluserglyglylyleuvallyleuuglyglyserleuylsleuser 21
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      141 gtgcacctggtgagctgggggagagcttgctcaacctggagagctccctgagacctctcc 200

```



Oy		22	CysAlaIalaSerGlyPheThrPheserAsnTyrTyrmetsertTPbAArgInThPro	41
Db		201	TGTCCAGCGCTTGGAATTACCTTCAGATCACTACATCATGACTGCATGCCAGAGCTCCA	260
Oy		42	GluYsarArgLeuGluLeuValAlaAlaIleasnerAspGlyGlyIethrTyrTyrleu	61
Db		261	GGGAAGGGCGCTGGAGTGGGTTTCATATTAAGTAGTAGTAGTACCATTACTACGCA	320
Oy		62	AspThrValIlygLyArgPheThrIleaserArgaPanalalyAsnThrleuTyrleu	81
Db		321	GACTCTGGAAAGGGCCGATTCACCATTCACGGAGCAACGCGCAAGATCCTGATATG	380
Oy		82	GlnmetSerSerLeuLYseSerglunAspThrIaleuPheTyrCySAlaArgHISArSer	101
Db		381	CAATGAACAACCTCAGAGCCGAGACACGGCCCGTATTTACTGTGGCAGAATACCCGGGT	440
Oy		102	Gly-----TyrPheserVetcapTyrTrpGlyGlnGlyThServalthr	116
Db		441	GGTAACCTCCTACTACTACTACGCGTATGAGCGTGGGGCGAAGGAGCACCGTACC	500
Oy		117	ValserSer	119
Db		501	GTCTCTCA	509
RESULT 14				
B7Y50520			667 bp	mRNA linear EST 17-DEC-2002
LOCUS				
DEFINITION			B7Y50520 RIKEN full-length enriched, activated spleen Mus musculus	
ACCESSION			CDNA clone F830004G20 5', mRNA sequence.	
VERSION			BY750520	
KEYWORDS			BY750520.1 GI:27180458	
SOURCE			EST.	
ORGANISM			Mus musculus (house mouse)	
			Mus musculus	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;	
			Schirognathi; Muroidae; Muridae; Murinae; Mus.	
REFERENCE			1 (bases 1 to 667)	
AUTHORS			Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Otsu,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bulc,C., Hune,D.A., Quackenbush,J., Schrimf,L.M., Kanapin,A., Matsumda,H., Bateola,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chochova,C., Corbani,L.E., Cousins,S., Datta,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Guestinch,C., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedierski,R.M., King,B.L., Konagaya,A., Kurachkin,I.V., Lee,Y., Lemhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.U., Petrea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,U.T., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempke,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,X., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Kohno,H., Nakamura,M., Sakizume,N., Satoh,K., Shiraki,T., Waki,K., Kawai,Y., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashigume,W., Imotani,K., Ishii,Y., Itomura,K., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shihata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)	
JOURNAL				
PUBMED				
COMMENT				
			Contact: Yoshihide Hayashizaki	
			Laboratory for Genome Exploration Research Group, RIKEN Genomic	
			Sciences Center(GSC), Yokohama Institute	
			The Institute of Physical and Chemical Research (RIKEN)	

```

1-7-22 Shunho-cho, Tsutsumi-ku, Yokohama, Kanagawa 230-0043, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, Y., Kagawa, K., Kawai, J., Kojima, Y.,
Kondo, S., Komori, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Nomazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/RNC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
source
Location/Qualifiers
1..667
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F830004G20"
/tissue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN
Alignment Scores:
Pred. No.: 7.53e-50 Length: 667
Score: 453.50 Matches: 91
Percent Similarity: 83.2% Conservative: 8
Best Local Similarity: 76.5% Mismatches: 19
Query Match: 73.5% Indels: 1
DB: 4 Gaps: 1
US-10-635-908-6 (1-119) x BY750520 (1-667)
QY 1 AspValIvsLeuValGIUsersrGIyGIyLeuValIvsLeuGIySeriLeuIvsLeu 20
::: :::
Db 131 GAAGTCACACTGTGTGAAGCTGGGGAGAGCTTAGTGAAGAGCCTGGAGGGCTCCGAAATC 190
QY 21 SerCysAlaIalasrGIyPheThrPheSerAntyTYrMetSerTTPValArgInThr 40
::: :::
Db 191 TCTGTGACAGCCTGTGATTCACCTTCAGTAGCTATGTCACATGCTGTGGGTGCGCAGCT 255
QY 41 ProGluIvsArgIvsLeuGIuLeuValAlaAlaIalasrAargIyGIyIleThrTYrTYr 60
::: :::
Db 251 CCGGAAGAGAGGCTGGAGGGCTCGCAACCATTAAGTATGGTGGTAAGTAACTACTAT 311
QY 61 LeuAspThrValIvsGIyArgPheThrIleserAgaAspAenAlaIvsAenThrLeuTYr 80
::: :::
Db 311 CCAGACAAATGTAAGGGCGGATTCACATCTCCAGAGCAATGCCAGAGCAACCTGTAC 370
QY 81 LeuGIuMetSerSerIvsLeuIvsSeriGluAspThrAlaIvsPheTYrCysAlaArgHisArg 100
::: :::

```

RESULT 15	AK156019	1565 bp	mRNA	linear	HTC 21-SEP-2005
LOCUS	AK156019				
DEFINITION	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:FE30004G20 product:immunoglobulin heavy chain 4 (sperm IgG1), full insert sequence.				
ACCESSION	AK156019				
VERSION	AK156019.1	GI:74217594			
KEYWORDS	HTC; CAP trapper.				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	10349666				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aikawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuwaki, N., Lewis, S., Matsuo, Y., Nishida, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gastlrich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaeerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyohara, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohzuki, S. and Hayashizaki, Y.				
CONSTRM	RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409 (6821), 685-690 (2001)				
PUBMED	11217851				
REFERENCE	5				
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Oshino, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,				
CONSTRM	FANTOM Consortium				
TITLE	The transcriptional landscape of the mammalian genome				
JOURNAL	Science 309 (5740), 1559-1563 (2005)				
PUBMED	16141072				
REFERENCE	7				
AUTHORS	Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M.,				

[illegible]



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 06:47:11 ; Search time 118.643 Seconds  
(without alignments)  
2815.117 Million cell updates/sec

Title: US-10-635-908-6  
Perfect score: 617  
Sequence: 1 DVKLTVSGGGLVTLGGSLKLT.....RSGYFMDYMGQGTSTVYSS 119

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Delop 6.0 , Delext 7.0

Searched: 1403666 segs, 935554401 residues  
Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abs/ABSSWB.spool/US10635908/runat\_02062006\_104220\_10327/app\_query.fasta\_1  
-Db=Issued Patents\_NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOFCU=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=plco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-HOST=absg02h -USER=US10635908 @CGN 1.1 252 @runat\_02062006\_104220\_10327  
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -KAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents\_NA:\*

1: /EMC\_Celerra\_SIDS3/prodata/2/ina/1 COMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/ina/5 COMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/ina/6A COMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/ina/6B COMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/ina/7 COMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/ina/7 COMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/ina/7 COMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/prodata/2/ina/7 COMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/prodata/2/ina/7 COMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/prodata/2/ina/7 COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	90.6	474	2	US-08-653-402B-5
2	559	90.6	474	2	US-08-653-402B-9
3	498	80.7	484	3	US-10-226-795-31
4	486.5	78.8	360	2	US-08-672-176A-1
5	479	77.6	717	2	US-08-553-497A-17
6	475.5	77.1	405	3	US-08-579-378A-15
7	474	76.8	3343	10	5453363-2
8	471	76.3	747	5	US-09-661-992B-83

9	470.5	76.3	888	5	US-09-661-992B-99	Sequence 99, Appl
10	470.5	76.3	978	5	US-09-661-992B-91	Sequence 91, Appl
11	470.5	76.3	2199	5	US-09-661-992B-89	Sequence 89, Appl
12	469	76.0	357	2	US-08-331-398A-21	Sequence 21, Appl
13	469	76.0	357	2	US-08-331-397B-21	Sequence 21, Appl
14	469	76.0	357	2	US-08-759-804A-21	Sequence 21, Appl
15	469	76.0	357	3	US-09-227-693-21	Sequence 21, Appl
16	469	76.0	375	2	US-08-331-398A-59	Sequence 59, Appl
17	469	76.0	375	2	US-08-331-397B-59	Sequence 59, Appl
18	469	76.0	375	2	US-08-759-804A-58	Sequence 58, Appl
19	468	75.9	414	2	US-08-379-057-13	Sequence 13, Appl
20	467	75.7	351	3	US-09-339-922A-5	Sequence 5, Appl
21	467	75.7	351	3	US-08-791-391A-5	Sequence 5, Appl
22	467	75.7	351	3	US-09-016-061-5	Sequence 5, Appl
23	465	75.4	923	7	PCT-US94-07659-1	Sequence 1, Appl
24	464.5	75.3	783	3	US-08-487-283A-19	Sequence 19, Appl
25	464	75.2	711	4	US-10-073-301A-8	Sequence 8, Appl
26	464	75.2	804	3	US-09-554-765-1	Sequence 1, Appl
27	463.5	75.1	372	3	US-09-518-737-1	Sequence 1, Appl
28	460.5	74.6	411	3	US-09-269-332-57	Sequence 57, Appl
29	460.5	74.6	1347	10	5455030-2	Sequence 57, Appl
30	460	74.3	717	2	US-07-956-399-3	Sequence 3, Appl
31	458.5	74.3	477	2	US-08-653-402B-1	Sequence 1, Appl
32	457.5	74.1	361	3	US-09-025-769B-62	Sequence 62, Appl
33	457.5	74.1	361	3	US-09-490-070A-62	Sequence 62, Appl
34	457.5	74.1	361	3	US-09-490-153-62	Sequence 62, Appl
35	457.5	74.1	361	3	US-09-490-324-62	Sequence 62, Appl
36	457.5	74.1	843	3	US-09-025-769B-177	Sequence 177, App
37	457.5	74.1	843	3	US-09-490-070A-177	Sequence 177, App
38	457.5	74.1	843	3	US-09-490-153-177	Sequence 0, Appl
39	457.5	74.1	843	3	US-09-490-324-177	Sequence 177, App
40	455.5	73.8	513	3	US-09-318-786-32	Sequence 32, Appl
41	452.5	73.3	747	5	US-09-661-992B-87	Sequence 87, Appl
42	451.5	73.2	747	5	US-09-661-992B-85	Sequence 85, Appl
43	451	73.1	357	2	US-08-475-000-15	Sequence 15, Appl
44	451	73.1	357	2	US-08-483-199-15	Sequence 15, Appl
45	451	73.1	357	2	US-08-484-508-15	Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
US-08-653-402B-5  
; Sequence 5, Application US/08653402B  
; Patent No. 5969107  
; GENERAL INFORMATION:  
; APPLICANT: CARCELLER, Ana  
; APPLICANT: ROSELL, Elisabet  
; APPLICANT: GOMEZ, Alicia  
; APPLICANT: ADEN, Jaume  
; APPLICANT: PIULATS, Jaume  
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an  
; NUMBER OF SEQUENCES: 13  
; IMMUNE response against epidermal growth factor receptor.  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
; STREET: 2200 Clarendon Boulevard, Suite 1400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (ERO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/653,402B  
; FILING DATE: 24-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95107967.2  
; FILING DATE: 26-MAY-1995

```

ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1781
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: monoclonal anti-idiotypic anti-EGFR antibody
INDIVIDUAL ISOLATE: 5A6 heavy chain
FEATURE:
NAME/KEY: CDS
LOCATION: 1..474
US-08-653-402B-5

Alignment Scores:
Pred. No.: 3,11e-65 Length: 474
Score: 559.00 Matches: 111
Percent Similarity: 92.8% Conservative: 5
Best Local Similarity: 98.8% Mismatches: 3
Query Match: 90.6% Indels: 6
DB: 2 Gaps: 2

US-10-635-908-6 (1-119) x US-08-653-402B-5 (1-474)
QY 1 AspyValysLeuValGluSerGlyGlyGlyLeuValLysLeuGlyGlySerLeuLysLeu 20
Db 58 GACGTGAAGCTCTGTGAGTCTGGGGGAGGCTTAGTGAACTTGGAGGGTCCCTGAACCTA 117
QY 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
Db 118 TCCTGTCAACCTCTGGATTCACTTCAGTAATTAATACATGTCCTGGGTTCCGACACT 177
QY 41 ProGluValArgLeuGluGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
Db 178 CCAGAGGAAGGCGCTGGAGTTGTGCGACGCAATTATAGTAAGTGGTAGACCTACTAT 237
QY 61 LeuAspThrValIlysgIyArpPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
Db 238 CCAGACACTGTGAAGGCGCATTCACCAATCTCCAGACAAATGCCAAGAACCCCTGTAC 297
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
Db 298 CTGCAAATGACAGTCTGAGTCTGAGGACACAGCCCTGTATCTATCTGGCAAGACATCGG 357
QY 101 -----SerGlyTyr-----PheSerMetAspTyrTyrTyrGlyGlyIleThrSer 114
Db 358 GCGAGGACACAGCTCGGGCTACGTAGAGGTATCTATAGACTACTGGGGTCAAGAACTCA 411
QY 115 ValThrValSerSer 119
Db 418 GTCACGCTCTCTCA 432

RESULT 2
US-08-653-402B-9
/ Sequence 9, Application US/08653402B
/ Patent No. 5969107
/ GENERAL INFORMATION:
/ APPLICANT: CARCELLER, Ana
/ APPLICANT: ROSELLI, Elisabet
/ APPLICANT: GOMEZ, Alicia
/ APPLICANT: ADEN, Jaume
/ APPLICANT: PIULATS, Jaume
/

```

```

1  TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
2  TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
3  NUMBER OF SEQUENCES: 13
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Millen, White, Zejano & Branigan, P.C.
6  STREET: 2200 Clarendon Boulevard, Suite 1400
7  CITY: Arlington
8  STATE: Virginia
9  COUNTRY: U.S.A.
10 ZIP: 22201
11
12 COMPUTER READABLE FORM:
13
14 MEDIUM TYPE: Floppy disk
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/653,402B
19 FILING DATE: 24-MAY-1996
20 CLASSIFICATION: 435
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: EP 95107967.2
24 FILING DATE: 26-MAY-1995
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Lepovitz, Richard M.
27 REGISTRATION NUMBER: 37,067
28 REFERENCE/DOCKET NUMBER: MERCK 1781
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 703-243-6333
31 TELEFAX: 703-243-6410
32 INFORMATION FOR SEQ ID NO: 9:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 474 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: cDNA
39 HYPOTHETICAL: NO
40 ANTI-SENSE: NO
41 FRAGMENT TYPE: N-terminal
42 ORIGINAL SOURCE:
43 ORGANISM: monoclonal anti-idiotypic anti-EGFR antibody
44 INDIVIDUAL ISOLATE: 3B6 heavy chain
45 FEATURE:
46 NAME/KEY: CDS
47 LOCATION: 1..474
48
49 US-08-653-402B-9
50
51 Alignment Scores:
52 Pred. No.:
53 Score: 3,11e-65 Length: 474
54 Percent Similarity: 559.00 Matches: 111
55 Best Local Similarity: 88.8% Mismatches: 5
56 Query Match: 90.6% Indels: 6
57 DB: 2 Gaps: 2
58
59 US-10-635-908-6 (1-119) x US-08-653-402B-9 (1-474)
60
61 QY 1 AspyAllylsuEuValIguSerGIyGIyLyuValLysLeuGIyGIySerLeuLyLeu 20
62 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
63 Db 58 GACSTGAAGCTCGTGAGCTCTGGGGGAGGCTTAGTGAAGCTTGGAGGGCTCCCGAAACTC 117
64 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
65 QY 21 SerCyAlaIaIaSerGIyPheThrPheSerAsnTyRTyMetSerTPValArgInThr 40
66 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
67 Db 118 TCGTGCGAGCGCTGTGATTCACCTTCAGTACTATTACATGCTTCGGATTGCCAGACT 177
68 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
69 QY 41 ProGluLySarGLeuGIuLeuValAlaAlaIleAsnSerAspGIyGIyIleThrTyTyr 60
70 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
71 Db 178 CCAAGAGGAGGGCTGGAGGTGTGTCGACGCCATTATATGTATGTGTGTAGCACCTACTAT 237
72 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
73 QY 61 LeuAspThrValLySGIyArgPheThrIleSerArgAspAsnAlaLyAsnThrLeuTyR 80
74 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
75 Db 238 CCAACACTGTGAAGGGCCCATTCACCATCTCCAGAGACATGCCAAGAACACCTCTTAC 297

```



VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 1:  
US-08-672-176A-1

Alignment Scores:  
Pred. No.: 9, 68e-56 Length: 360  
Score: 486.50 Matches: 98  
Percent Similarity: 89.3% Conservatave: 11  
Best Local Similarity: 80.3% Mismatches: 8  
Query Match: 78.8% Indels: 5  
DB: 2 Gaps: 2

US-10-635-908-6 (1-119) x US-08-672-176A-1 (1-360)

QY 1 AspValLysLeuValGluSerGlyGlyLeuValLysLeuGlyGlySerLeuLysLeu 20  
1 GAGGTGACAGCTGTGAGTCTGGGGAGGCTTAGTGACAGCTGGAGGCTCCCTGAAACCTC 60  
DB 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40  
61 TCCTGTGACAGCTGTGAGTCTGATTCATTCTATGCGATGCTTGCGGTGCGCAGACT 120  
QY 41 ProGluLysArgLeuGluLeuValAlaAlaAlaLeuSerAspGlyGlyLeuThrTYrTYr 60  
121 CCAGACAAAGAGCTGGAGTGGTCGCGACACATTAAATAGTAATGGTGTAAACCTATTAT 180  
QY 61 LeuAspThrValLysGlyValArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTYr 80  
181 CCAGACAGGTGTGAAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCTCTGTAC 240  
QY 81 LeuGlnMetSerSerLeuLysSerGlyAspThrAlaLeuPheTYrCyAlaArgHisArg 100  
241 CTGCATTAAGACGCTGAGTGTGAGTGTGAGACACAGCATGATTACTGTGCA-----AGA 294  
DB 101 SerGly-----TYrPheSerMetAspTYrTYrGlyGlnGlyThrSerValThrVal 117  
295 GATGGTACCTTATTACTATGCTATGACTACTGCGGTCAAGAAACCTCAGTCAACGCTC 354  
QY 118 SerSer 119  
DB 355 TCCTCA 360

RESULT 5  
US-08-553-497A-17  
Sequence 17, Application US/08553497A  
Patent No. 5844093  
GENERAL INFORMATION:  
APPLICANT: KETTLERBOROUGH, C. A.  
APPLICANT: BENDIG, MARY M.  
APPLICANT: ANGELL, KEITH H.  
APPLICANT: GUSSON, DETLEF  
APPLICANT: ADAM, JAUME  
APPLICANT: MIRJANS, FRANCESCA  
APPLICANT: ROSELL, ELISABET  
APPLICANT: BLASCO, FRANCESC  
APPLICANT: PILATS, JAUME  
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0  
FILING DATE: 17-MAR-1994  
PRIOR APPLICATION DATA: EP 94118970.6  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1726  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 717 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: mouse  
STRAIN: Balb/c  
DEVELOPMENTAL STAGE: adult  
TISSUE TYPE: splenocytes  
IMMEDIATE SOURCE:  
CLONE: 4 B 2  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..717  
US-08-553-497A-17

Alignment Scores:  
Pred. No.: 2, 53e-54 Length: 717  
Score: 479.00 Matches: 93  
Percent Similarity: 88.2% Conservatave: 12  
Best Local Similarity: 78.2% Mismatches: 14  
Query Match: 77.6% Indels: 0  
DB: 2 Gaps: 0

US-10-635-908-6 (1-119) x US-08-553-497A-17 (1-717)

QY 1 AspValLysLeuValGluSerGlyGlyLeuValLysLeuGlyGlySerLeuLysLeu 20  
1 GAGGTGACAGCTGTGAGTCTGGGGAGGCTTAGTGACAGCTGGAGGCTCCCTGAAACCTC 60  
DB 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40  
61 TCCTGTGACAGCTGTGAGTCTGATTCATTCTATGCGATGCTTGCGGTGCGCAGACT 120  
QY 41 ProGluLysArgLeuGluLeuValAlaAlaAlaLeuSerAspGlyGlyLeuThrTYrTYr 60  
121 CCAGACAAAGAGCTGGAGTGGTCGCGACACATTAAATAGTAATGGTGTAAACCTATTAT 180  
QY 61 LeuAspThrValLysGlyValArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTYr 80  
181 CCAGACAGGTGTGAAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCTCTGTAC 240  
QY 81 LeuGlnMetSerSerLeuLysSerGlyAspThrAlaLeuPheTYrCyAlaArgHisArg 100



Db 241 CCGCAATATGACGCTGTGAAGTGTGAGACACAGCCATGATATGCTGCAAGACTTGAA 300

QY 101 SerGlyTYrPheSerMetAspTYrTPGlyGlyGlyThrservalThrValSerSer 119  
 Db 301 ACCGGGAGACTATGCTTGTGACTACTGGGCGCAAGGACGAGTCACTCTCTCTCA 357

## RESULT 6

US-08-579-378A-15  
 ; Sequence 15, Application US/08579378A  
 ; Patent No. 6210671

GENERAL INFORMATION:  
 APPLICANT: Co, Man Sung  
 TITLE OF INVENTION: Humanized Antibodies Reactive with  
 TITLE OF INVENTION: L-Selectin  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew  
 STREET: One Market Plaza, Steuart Tower, Suite 2000  
 City: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94105

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/579,378A  
 FILING DATE: 27-DEC-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/160,074  
 FILING DATE: 30-NOV-1993

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/983,946  
 FILING DATE: 01-DEC-1992

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 95112895.8  
 FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 95114696.8  
 FILING DATE: 19-SEP-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Liebescheutz, Joe O.  
 REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 11823-002220  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-326-2400  
 TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 405 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..405

US-08-579-378A-15

Alignment Scores:

Pred. No.: 3.33e-54 Length: 405  
 Score: 475.50 Matches: 95  
 Percent Similarity: 88.2% Conservative: 10  
 Best Local Similarity: 79.8% Mismatches: 11  
 Query Match: 77.1% Indels: 3  
 DB: 3 Gaps: 2

US-10-635-908-6 (1-119) x US-08-579-378A-15 (1-405)

Db 1 AspValIysLeuValIgluSerGlyGlyLeuValIysLeuGlyGlySerLeuIysLeu 20

QY 58 GAAGTGAAGAGCTGTGAGTGTGGGAGAGCTTGAAGAGCTGGAGGGCTCTGAAATCTC 117

Db 21 SerCysAlaIaIaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40

QY 118 GCCTGTGCCCTCTGGATTCACTTCACTTCACTTATGCCATGTCTTGGTTGCCAGACT 177

Db 41 ProGluIysArgLeuGluIleuValIaIaIaIeasSerAspGlyIleThrTYrTYr 60

QY 178 CCAGAGAAAGAGCTGTGAGTGTGGGAGAGCTTGAAGAGCTGGAGGGCTCTGAAATCTC 234

Db 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTYr 80

QY 235 CCAGACAGTGTGAAGGCGGATTCACCATCTCCAGAGATTAATGCCAGAACTCTGTAC 294

Db 81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTYrCysAlaArgHisArg 100

QY 295 CCGCAATATGACGCTGTGAAGTGTGAGACACAGCCATGATATGCTGCAAGACTTGAA 354

QY 101 SerGlyTYrPheSerMetAspTYrTPGlyGlyGlyThrservalThrValSerSer 119

Db 355 GACGGGTATTTT-----GACTACTGGGGCAAGCAGCAGCTCTCAGCTCTCTCA 405

RESULT 7

5453363-2

Patent No. 5453363

APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RAUF

TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR

ING AFTER GENETIC EXPRESSION IN PROKARYOTES

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/206,044

FILING DATE: 02-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 942,370

FILING DATE: 09-SEP-1992

APPLICATION NUMBER: 498,500

FILING DATE: 23-MAR-1990

APPLICATION NUMBER: 76,207

FILING DATE: 23-OCT-1986

SEQ ID NO: 2

LENGTH: 3343

Alignment Scores:

Pred. No.: 1e-52 Length: 3343

Score: 474.00 Matches: 94

Percent Similarity: 85.4% Conservative: 11

Best Local Similarity: 76.4% Mismatches: 14

Query Match: 76.8% Indels: 4

DB: 10 Gaps: 1

US-10-635-908-6 (1-119) x 5453363-2 (1-3343)

QY 1 AspValIysLeuValIgluSerGlyGlyLeuValIysLeuGlyGlySerLeuIysLeu 20

Db 240 GAAGTTCAGAGTGTGAGTGTGGGAGAGCTTGAAGAGCTGGAGGGCTCTGAAATCTC 299

QY 21 SerCysAlaIaIaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40

Db 300 TCCGTGTCCAGCTCTGTGATTCATCTTCACTTATTAATGATTTGGTTGCCAGACT 359

QY 41 ProGluIysArgLeuGluIleuValIaIaIaIeasSerAspGlyIleThrTYrTYr 60

Db 360 CCGGAAAAGAGCTGTGAGTGTGGGAGAGCTTGAAGAGCTGGAGGGCTCTGAAATCTC 419

QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTYr 80

Db 420 CCAGACAGTGTGAAGGCGGATTCACCATCTCCAGAGATTAATGCCAGAACTCTGTAC 479

QY 81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTYrCysAlaArgHisArg 100

Db		480	CTGCAGAAATGACGACTGTGAAGTCTGATGACACAGCCATGATATTACTGTGCAAGAAGATAAG	539
OY		101	SerGIgLYr-----PheSerMetAspTYrTrIGIyGINgIyThrservValThr	116
Db		540	GCGTTCTATTAGTGTAACACTACGGCAGTCATGCTATGAGACTACTGGGGGTCAAGAAACCTCAGTCACC	599
OY		117	ValSerSer 119 	
Db		600	GTCTCTCTCA 608 	
		RESULT 8		
		US-09-661-992B-83		
	/	Sequence 83, Application US/09661992B		
	/	Patent No. 7033590		
	/	GENERAL INFORMATION:		
	/	APPLICANT: Schefflinger, Friedrich		
	/	APPLICANT: Kerschbaumer, RandoIf		
	/	APPLICANT: Falkner, Falko-Guenther		
	/	APPLICANT: Dornier, Friedrich		
	/	APPLICANT: Baxter Aktiengesellschaft		
	/	TITLE OF INVENTION: Factor IXA Activating Antibodies and Antibody		
	/	FILE REFERENCE: Derivatives		
	/	CURRENT APPLICATION NUMBER: US/09/661,992B		
	/	CURRENT FILING DATE: 2000-09-14		
	/	PRIOR APPLICATION NUMBER: AT A157600		
	/	PRIOR FILING DATE: 1999-09-14		
	/	NUMBER OF SEQ ID NOS: 112		
	/	SOFTWARE: PatentIn Ver. 2.1		
	/	SEQ ID NO: 83		
	/	LENGTH: 747		
	/	TYPE: DNA		
	/	ORGANISM: Artificial Sequence		
	/	FEATURE:		
	/	OTHER INFORMATION: Description of Artificial Sequence: scFv from		
	/	OTHER INFORMATION: hybridoma cell line 193/KZ		
		US-09-661-992B-83		
		Alignment Scores:		
		Pred. No.: 3,11e-53 Length: 747		
		Score: 471.00 Matches: 95		
		Percent Similarity: 86.0% Conservative: 9		
		Best Local Similarity: 76.5% Mismatches: 15		
		Query Match: 76.3% Indels: 2		
		DB: 5 Gaps: 2		
		US-10-635-908-6 (1-119) x US-09-661-992B-83 (1-747)		
OY		1	AapValIysLeuValGIsuSerGIyGIyLLeuValIysLeuGIySertLeuIysLeu	20
		:::::		
Db		1	GAAGTGCACACTGGTGTGAGCTGTGGGGGAGGCTTAGTGAAGCTGTGAAGGCTCCGTGAATCTC	60
OY		21	SerCYeAlAlaIasergIyphetrPheserAsnTYrTywetsertIpValArgGIIntHr	40
Ddb		61	TCTGTGCAAGCCCTCTGGAATTCACTTCAGTACTATACCATGTCTTGGGGTCCCGAGACT	120
OY		41	ProGIuLyArgIeuGIuLeuValAlaIaleasnseraspGIyLIetHrTYr	60
		:::::		
Db		121	CCGGAGAAAGAGGCTGAGGTGGGTGCCAACATTAGTAGTGCTGGTAGTACACCTACTAT	180
OY		61	LeuAspTHrValIysGIyArGPhetHrIIseSerArgspAsnAlalySaenHrLeuTYr	80
		:::::		
Db		181	CCAGACAGGTGTGAGGGGCCGATTCAACATCTCCAGAGACAATGCCAAGAACACCCCTGTAC	240
OY		81	LeuGIuMeSerSertLeuIysSerGIuAspTHrAlAleuPheTYrCySalatIGHISArg	1000
		:::::		
Db		241	CTGCAGAAATGACGACTGTGAAGTCTGAGACACAGCCAATGATTACTGTACAAAGATGGG	3000
OY		101	Ser---GI TYr---PheSerMetAspTYrTrIGIyGINgIyThrservValThrValSer	118
		:::::		
Db		301	GGACACGGGTACCGGTAGTACTTTGACTACTGGGGGCCAAGGACACACTCTCACAGTCTCC	3600
OY		119	Ser 119	

```

Db          361 TCA 363
|||||
RESULT 9
US-09-661-992B-99
; Sequence 99, Application US/09661992B
; Patent No. 7033590
; GENERAL INFORMATION:
; APPLICANT: Schefflinger, Friedrich
; APPLICANT: Kerschbaumer, Randoif
; APPLICANT: Falkner, Falko-Guenther
; APPLICANT: Dornier, Friedrich
; APPLICANT: Baxker Aktiengesellschaft
; TITLE OF INVENTION: Factor IX/Factor Ixa Activating Antibodies and Antibody
; TITLE OF INVENTION: Derivatives
; FILE REFERENCE: 20695C-005900US
; CURRENT APPLICATION NUMBER: US/09/661,992B
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: At A15/600
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:198AB2 scFv
; OTHER INFORMATION: linked to c-myc-tag and His6 tag (ORF of
; OTHER INFORMATION: expression vector pMyChis6-198AB2#102)
; FEATURES:
; NAME/KEY: modified_base
; LOCATION: (228)
; OTHER INFORMATION: n = g, a, c o r t
US-09-661-992B-99

Alignment Scores:
Pred. No.: 4,62e-53 Length: 888
Score: 470.50 Matches: 94
Percent Similarity: 84.4% Conservative: 9
Best Local Similarity: 77.0% Mismatches: 16
Query Match: 76.3% Indels: 3
DB: 5 Gaps: 1

US-10-635-908-6 (1-119) x US-09-661-992B-99 (1-888)
QY 1 AspValysLeuValGluSerGlyGlyLeuValLysLeuGlyGlySerLeuLysLeu 20
Db :::: 470.50 Matches: 94
67 GAGTGAAGAGCTGTGTGAGCTGTGGGGAGGCTTAGTGAAGCTTGAGAGGCTCCGAAATC 126
QY 21 SerCysAlaIAsSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40
Db :::: 470.50 Matches: 94
127 TCCTGTGACGCTCTGGATTCACTTTCATAGCTATACCATGTCTTGGGTCCGACACT 166
QY 41 ProGlyuSarGLeuGluLeuValAlaAlaIAsnSerAspGlyGlyIleThrTyrTyr 60
Db :::: 470.50 Matches: 94
167 CCGAGGAAGAGGCTGGAGTGGGTCCGAACCATTAGTAGTGNGNGTAGTCCACTACTAT 246
QY 61 LeuAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
Db :::: 470.50 Matches: 94
247 CCAGACAGGTGAAGGGCCGATTCCATCTCCAGAGCAATGCCAAGAACACCCTGTAC 306
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
Db :::: 470.50 Matches: 94
307 CTGCAAAATGACGAGCTGTAGTCTGTAGAGCACAGCCATGATATTACTGTACAAGAGGG 366
QY 101 SerGlyTyr-----PheSerMetAspTyrTrpGlyGlnGlyThrSerValThrVal 117
Db :::: 470.50 Matches: 94
367 GGTGGTTTCACCGTCAACTGTATCGATTGTCGTGGGGCGAGGAACCTCAGTACCAGTC 426
QY 118 SerSer 119
Db :::: 470.50 Matches: 94
427 TCCTCA 432

```

```
RESULT 10
US-09-661-992B-91
; Sequence 91, Application US/09661992B
; Patent No. 7033590
; GENERAL INFORMATION:
; APPLICANT: Schefflinger, Friedrich
; APPLICANT: Kerschbaumer, RandoIf
; APPLICANT: Falkner, Falko-Guenther
; APPLICANT: Dörner, Friedrich
; APPLICANT: Baxter Aktiengesellschaft
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody
; FILE REFERENCE: 20695C-005900US
; CURRENT APPLICATION NUMBER: US/09/661,992B
; CURRENT FILING DATE: 2000-09-14
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
; NAME/KEY: modified_base
; LOCATION: (1)..(978)
; OTHER INFORMATION: n = g, a, c or t
US-09-661-992B-91

Alignment Scores:
Pred. No.: 5,29e-53 Length: 978
Score: 470.50 Matches: 94
Percent Similarity: 84.4% Conservative: 9
Best Local Similarity: 77.0% Mismatches: 16
Query Match: 76.3% Indels: 3
DB: Gaps: 1

US-10-635-908-6 (1-119) x US-09-661-992B-91 (1-978)
QY 1 AspyVallylsleuValGlsuSerGlyGlyleuVallylsleuGlySerleuLysleu 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 67 GAGGTGAAGCTGTGGAGCTCTGGGGAGGCTTGAAGCCTGAGGGTCCCTGAATC 126
QY 21 SerCysAlaIaserglyPheThrPheSerAntyTyrrMetSerTrpValArgGlnThr 40
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 127 TCCTGTGACGCTCTGGATTCATTCTAGTATACCATGCTTGGGTTCCGACACT 186
QY 41 ProGluysArgleuGluLeuValAlaAlaIleasnsersaspGlyIleThrTyrr 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 187 CCGGAGAAGAGGCTGGAGTGGTGCACCATTAAGTAGTGAGGAGTTCACCTACTAT 246
QY 61 LeuaspThrVallysglyArgPheThrIleSerArgspAsnAlaLysAsnThrleuTy 80
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 247 CCAGACAGTGAAGGGCCGATTCACCATCTCCAGAGCAATGCCAAGAACCTCTGAC 306
QY 81 LeuGlnMetSerSerleuLysSerGluAspThrAlaLeuPheTyrrCysAlaArgHisArg 100
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 307 CTGCAAAATGACAGCTCTGAGCTCTGAGGACACAGCCATGATTAAGTACAAAGAGGGG 366
QY 101 SerGlyTyrr-----PheSerMetaspTyrrTrpGlyGlnGlyThrSerValThrVal 117
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 367 GGTGGTTTCACCGTCACACTGTGATCTTGATGTCTGGGGGCGCAGGAACCTCAGTCACCGTC 426
QY 118 SerSer 119
   |||||
DB 427 TCCTCA 432

RESULT 11
US-09-661-992B-89
```

```
; Sequence 89, Application US/09661992B
; Patent No. 7033590
; GENERAL INFORMATION:
; APPLICANT: Schefflinger, Friedrich
; APPLICANT: Kerschbaumer, RandoIf
; APPLICANT: Falkner, Falko-Guenther
; APPLICANT: Dörner, Friedrich
; APPLICANT: Baxter Aktiengesellschaft
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody
; FILE REFERENCE: 20695C-005900US
; CURRENT APPLICATION NUMBER: US/09/661,992B
; CURRENT FILING DATE: 2000-09-14
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 2199
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:198A2
; OTHER INFORMATION: scFv-alkaline phosphatase fusion protein (ORF of
; OTHER INFORMATION: expression vector pDAP2-198AB2#100)
; NAME/KEY: modified_base
; LOCATION: (228)
; OTHER INFORMATION: n = g, a, c or t
US-09-661-992B-89

Alignment Scores:
Pred. No.: 1,64e-52 Length: 2199
Score: 470.50 Matches: 94
Percent Similarity: 84.4% Conservative: 9
Best Local Similarity: 77.0% Mismatches: 16
Query Match: 76.3% Indels: 3
DB: Gaps: 1

US-10-635-908-6 (1-119) x US-09-661-992B-89 (1-2199)
QY 1 AspyVallylsleuValGlsuSerGlyGlyleuVallylsleuGlySerleuLysleu 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 67 GAGGTGAAGCTGTGGAGCTCTGGGGAGGCTTGAAGCCTGAGGGTCCCTGAATC 126
QY 21 SerCysAlaIaserglyPheThrPheSerAntyTyrrMetSerTrpValArgGlnThr 40
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 127 TCCTGTGACGCTCTGGATTCATTCTAGTATACCATGCTTGGGTTCCGACACT 186
QY 41 ProGluysArgleuGluLeuValAlaAlaIleasnsersaspGlyIleThrTyrr 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 187 CCGGAGAAGAGGCTGGAGTGGTGCACCATTAAGTAGTGAGGAGTTCACCTACTAT 246
QY 61 LeuaspThrVallysglyArgPheThrIleSerArgspAsnAlaLysAsnThrleuTy 80
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 247 CCAGACAGTGAAGGGCCGATTCACCATCTCCAGAGCAATGCCAAGAACCTCTGAC 306
QY 81 LeuGlnMetSerSerleuLysSerGluAspThrAlaLeuPheTyrrCysAlaArgHisArg 100
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 307 CTGCAAAATGACAGCTCTGAGCTCTGAGGACACAGCCATGATTAAGTACAAAGAGGGG 366
QY 101 SerGlyTyrr-----PheSerMetaspTyrrTrpGlyGlnGlyThrSerValThrVal 117
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 367 GGTGGTTTCACCGTCACACTGTGATCTTGATGTCTGGGGGCGCAGGAACCTCAGTCACCGTC 426
QY 118 SerSer 119
   |||||
DB 427 TCCTCA 432

RESULT 12
US-08-331-398A-21
; Sequence 21, Application US/08331398A
; Patent No. 5608039
```



US-10-635-908-6 (1-119) x US-08-331-397B-21 (1-357)

QY 1 AspVallylsleuValgluSerGlyglYglYleuVallylsleuGlySerleuLysLeu 20  
DB 1 GAGGTAAAGCTGGTGAATCTGAGAGGAGGCTTAGTGACAGCTGAGAGGCTCCGAAACTC 60

QY 21 SerCyAlaAlaIAserGlyPheThrPheSerAsnTyrrYmeSerTrpValArgInThr 40  
DB 61 TCCTGTGCAACCTCTGATTACTTTCAGTACATTAATGATGGGTCCAGACT 120

QY 41 ProGluLyArgleuGluLeuValAlaAlaIleAsnSerAspGlyglYleThrTyrrYr 60  
DB 121 CCAGAGAAAGAGCTGGAGTGGTGCATACATTAGTATGCTGTGACACCTATAT 180

QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTy 80  
DB 181 CCAGACACTGTAAAGGCGCATTCACCATCTCCAGAGACAACGCAAGAACCCGTGTAC 240

QY 81 LeuGlnMeSerSerleuLysSerGluAspThrAlaLeuPheTyrrCyAlaArgHisArg 100  
DB 241 CTCGACATGAGCCGCTGAGAGTCTGAGAGACACAGCCATGATATCTGCAAGGGGGCTC 300

QY 101 SerGlyTyrrPheSerMetAspTyrrTrpGlyGlnGlyThrservalThrValSerSer 119  
DB 301 TCTGATGCTTCTGTGTTGCTTACTGTGGGCCAAGGAGCTGTGCTACTGCTCTCA 357

RESULT 14  
US-08-759-804A-21  
Sequence 21, Application US/08759804A  
Patent No. 5990296  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Williamson, Mark  
APPLICANT: Fitzgerald, David J.  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Pal, Lee  
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,  
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,804A  
FILING DATE: 03-DEC-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/331,398  
FILING DATE: 28-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-126140US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:

LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY:  
LOCATION: 1..357  
OTHER INFORMATION: /note= "B5 Variable Heavy chain (V-H)"

US-08-759-804A-21

Alignment Scores:  
Pred. No.: 2.05e-53  
Score: 469.00  
Percent Similarity: 84.9%  
Best Local Similarity: 79.0%  
Query Match: 76.0%  
DB: 2  
Length: 357  
Matches: 94  
Conservative: 7  
Mismatch: 18  
Indels: 0  
Gaps: 0

US-10-635-908-6 (1-119) x US-08-759-804A-21 (1-357)

QY 1 AspVallylsleuValgluSerGlyglYglYleuVallylsleuGlySerleuLysLeu 20  
DB 1 GAGGTAAAGCTGGTGAATCTGAGAGGAGGCTTAGTGACAGCTGAGAGGCTCCGAAACTC 60

QY 21 SerCyAlaAlaIAserGlyPheThrPheSerAsnTyrrYmeSerTrpValArgInThr 40  
DB 61 TCCTGTGCAACCTCTGATTACTTTCAGTACATTAATGATGGGTCCAGACT 120

QY 41 ProGluLyArgleuGluLeuValAlaAlaIleAsnSerAspGlyglYleThrTyrrYr 60  
DB 121 CCAGAGAAAGAGCTGGAGTGGTGCATACATTAGTATGCTGTGACACCTATAT 180

QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTy 80  
DB 181 CCAGACACTGTAAAGGCGCATTCACCATCTCCAGAGACAACGCAAGAACCCGTGTAC 240

QY 81 LeuGlnMeSerSerleuLysSerGluAspThrAlaLeuPheTyrrCyAlaArgHisArg 100  
DB 241 CTCGACATGAGCCGCTGAGAGTCTGAGAGACACAGCCATGATATCTGCAAGGGGGCTC 300

QY 101 SerGlyTyrrPheSerMetAspTyrrTrpGlyGlnGlyThrservalThrValSerSer 119  
DB 301 TCTGATGCTTCTGTGTTGCTTACTGTGGGCCAAGGAGCTGTGCTACTGCTCTCA 357

RESULT 15  
US-09-227-693-21  
Sequence 21, Application US/09227693  
Patent No. 6287562  
GENERAL INFORMATION:  
APPLICANT: PASTAN, Ira  
APPLICANT: BENHAR, Itai  
APPLICANT: PADLAN, Eduardo A.  
APPLICANT: JUNG, Sun-Hee  
APPLICANT: LEE, ByungKook  
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY  
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khouie and Crew  
STREET: Steuart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/227,693  
FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/331,396  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-126-1-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..357  
OTHER INFORMATION: /standard\_name="B5"  
OTHER INFORMATION: variable heavy chain"  
US-09-227-693-21

Alignment Scores:  
Pred. No.: 2,05e-53 Length: 357  
Score: 469.00 Matches: 94  
Percent Similarity: 84.9% Conservative: 7  
Best Local Similarity: 79.0% Mismatches: 18  
Query Match: 76.0% Indels: 0  
DB: 3 Gaps: 0

US-10-635-908-6 (1-119) x US-09-227-693-21 (1-357)

QY 1 AspValIyleuValIgluSerGIYGIYLeuValIyleuGIYserLeuYsLeu 20  
:::|||||  
DB 1 GAGGTGAAGCTGTGGATCTGAGAGGAGCTTAGTGACGCTGGAGGTCCTGAACATC 60  
QY 21 SerCYAlAlAlaserGIYpHeThrPheSerAsnTYTYMeSerTrpValArgGlnThr 40  
|||||  
DB 61 TCCTGTGCAACCTCTGATTTACTTTCAGTACTATTACATGATTGGGTTCCGACAGACT 120  
QY 41 ProGluIysArgIleuGIuLeuValAlAlAlAlAsnSerAspGIYGIYIleThrTYTYr 60  
|||||  
DB 121 CAGAGAGAGGCTGGAGTGGGTGCATACATTAATGATGATGATGATGATGATGAT 180  
QY 61 LeuAspThrValIysGIYArgPheThrIleSerArgAspAsnAlAlYsAsnThrLeuTYr 80  
|||||  
DB 181 CCAGACACTGTAAAGGCCGATTCAACATCTCCAGAGACAAAGCCAAACACCTGTAC 240  
QY 81 LeuGIYMeSerSerIleuIysSerGIYAspThrAlAlAlAlAlAlAlAlAlAlAlAl 100  
|||||  
DB 241 CTGCACATGAGCCGCTGTAAGTCTGAGGACACAGCCATGATTAATGATGATGATGAT 300  
QY 101 SerGIYTYrPheSerMetAspTYrTrpGIYGIYGIYThrSerValThrValSerSer 119  
|||||  
DB 301 TCTGATGTTCTGCTGTTGCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357

Search completed: June 3, 2006, 06:53:41  
Job time: 121.643 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 06:54:05 ; Search time 817.991 Seconds  
(without alignments)  
2681.378 Million cell updates/sec

Title: US-10-635-908-6  
Perfect score: 617  
Sequence: 1 DVKLVEGSGGLVKGSLKLT.....RSGYFSMDYWGQTSVTSS 119

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues  
Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-Qc/abses/ABSSWEB.spool/US10635908/runat.02062006.104222.10380/app.query.fasta\_1  
-DB=Published Applications NA.Mam -OPMT=fastap -SUFIX=xnpbm -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsu62  
-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=abs802h  
-USER=US10635908.@CGN\_1.1.2326.@runat.02062006.104222.10380 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.Main.\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_PUBCOMB.seq.\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_PUBCOMB.seq.\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_PUBCOMB.seq.\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result Query Match Length DB ID Description  
No. Score  
1 617 100.0 357 8 US-10-470-940-1 Sequence 1, Appli

2 617 100.0 357 9 US-10-635-908-5 Sequence 5, Appli  
3 617 100.0 1056 8 US-10-333-235A-8 Sequence 8, Appli  
4 617 100.0 1411 8 US-10-333-235A-10 Sequence 10, Appli  
5 617 100.0 1702 8 US-10-333-235A-11 Sequence 11, Appli  
6 617 100.0 2431 9 US-10-635-908-9 Sequence 9, Appli  
7 605 98.1 444 11 US-10-504-189A-50 Sequence 50, Appli  
8 498 80.7 484 8 US-10-226-795-31 Sequence 31, Appli  
9 495 80.2 466 3 US-09-881-823-11 Sequence 11, Appli  
10 495 80.2 533 3 US-09-910-358D-5 Sequence 5, Appli  
11 495 80.2 533 8 US-10-077-624-5 Sequence 5, Appli  
12 495 80.2 533 8 US-10-706-391-3 Sequence 3, Appli  
13 495 80.2 563 3 US-09-910-358D-1 Sequence 1, Appli  
14 495 80.2 563 7 US-10-077-624-1 Sequence 1, Appli  
15 495 80.2 563 8 US-10-706-391-1 Sequence 1, Appli  
16 482 78.1 374 7 US-10-169-351-66 Sequence 66, Appli  
17 482 78.1 756 7 US-10-169-351-68 Sequence 68, Appli  
18 481 78.0 1386 7 US-10-281-479A-21 Sequence 21, Appli  
19 481 78.0 1386 7 US-10-286-132A-21 Sequence 21, Appli  
20 481 78.0 1398 7 US-10-275-180A-21 Sequence 21, Appli  
21 480.5 77.9 360 8 US-10-383-447-5 Sequence 5, Appli  
22 478 77.5 363 7 US-10-300-215-88 Sequence 8, Appli  
23 478 77.5 369 10 US-10-490-535-1 Sequence 1, Appli  
24 478 77.5 420 3 US-09-286-240-3 Sequence 3, Appli  
25 472 76.5 414 7 US-10-010-942B-3 Sequence 3, Appli  
26 472 76.5 414 8 US-10-388-389-3 Sequence 3, Appli  
27 472 76.5 414 8 US-10-703-713-3 Sequence 3, Appli  
28 472 76.5 414 8 US-10-704-070-3 Sequence 3, Appli  
29 472 76.5 414 9 US-10-232-030-3 Sequence 3, Appli  
30 472 76.5 414 10 US-10-789-273-3 Sequence 3, Appli  
31 471 76.3 747 13 US-11-093-103-83 Sequence 83, Appli  
32 470.5 76.3 888 13 US-11-093-103-99 Sequence 99, Appli  
33 470.5 76.3 978 13 US-11-093-103-91 Sequence 91, Appli  
34 470.5 76.3 2199 13 US-11-093-103-89 Sequence 89, Appli  
35 468 75.9 366 7 US-10-258-728-1 Sequence 1, Appli  
36 467.5 75.8 746 8 US-10-354-246-3 Sequence 3, Appli  
37 467 75.7 351 2 US-08-790-540A-5 Sequence 5, Appli  
38 467 75.7 351 3 US-08-791-391A-5 Sequence 5, Appli  
39 467 75.7 351 3 US-09-900-590-5 Sequence 5, Appli  
40 467 75.7 351 7 US-10-305-231-5 Sequence 5, Appli  
41 467 75.7 351 7 US-10-452-440-5 Sequence 5, Appli  
42 467 75.7 351 7 US-10-463-847-5 Sequence 5, Appli  
43 467 75.7 351 10 US-10-959-871-5 Sequence 5, Appli  
44 465 75.4 345 8 US-10-436-782-45 Sequence 45, Appli  
45 465 75.4 345 8 US-10-436-783-13 Sequence 13, Appli

## ALIGNMENTS

RESULT 1  
US-10-470-940-1  
; Sequence 1, Application US/10470940  
; Publication No. US20040077081A1  
; GENERAL INFORMATION:  
; APPLICANT: Oosterwijk, Egbert  
; APPLICANT: Wernaar, Sven  
; APPLICANT: Ullrich, Stefan  
; TITLE OF INVENTION: Hybridoma Cell Line G250 and its use for producing monoclonal  
; TITLE OF INVENTION: antibodies  
; FILE REFERENCE: 2923-0548  
; CURRENT APPLICATION NUMBER: US/10/470, 940  
; CURRENT FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: PCT/ EP02/ 01282  
; PRIOR FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: US 60/ 266853  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: US 60/ 327008  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 357  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

```
FEATURE:
/ OTHER INFORMATION: mouse/human chimeric antibody gene
/
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(357)
/
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (91)..(105)
/ OTHER INFORMATION: sequence coding for the complementary determining region
/
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (148)..(198)
/ OTHER INFORMATION: sequence coding for the complementary determining region
/
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (295)..(324)
/ OTHER INFORMATION: sequence coding for the complementary determining region
/
US-10-470-940-1

Alignment Scores:
Pred. No.: 3,61e-76 Length: 357
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-635-908-6 (1-119) x US-10-470-940-1 (1-357)

QY 1 AspVallyLLeuValIGluserGlyGlyLeuValLlyLeuGlyGlySerLeuLysLeu 20
DB 1 GACGTGAAGCTGCTGAGCTGCGGGAGGCTTAGTGAAGCTTGAGAGGCTCCCTGAACCTC 60
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40
DB 61 TCCTGTGACGCTCTGAGATTCACTTCACTAATTAATGATGCTGGGTTGCGCAGACT 120
QY 41 ProGluLybArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60
DB 121 CCAGAGAAAGAGCTGAGAGTGTGCGACGCAATTAATGATGATGATGATACCTACTAT 180
QY 61 LeuAspThrValLlyGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTYr 80
DB 181 CTAGACACTGTGAAGGCGGATTCACATTTCAAGAGCAAGCCAGAACCTCTGATC 240
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTYrCYsAlaArgHisArg 100
DB 241 CTGCAATGAGAGCTGAGAGTCTGAGACACAGCCTTGTTTTACTGTGCAAGACACCGC 300
QY 101 SerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 301 TCGGGCTACTTTTCTATGAGCTACTGGGGTCAAGAACTCAAGTACCGTCTCTCA 357

RESULT 2
US-10-635-908-5
/ Sequence 5, Application US/10635908
/ Publication No. US20040219633A1
/ GENERAL INFORMATION:
/ APPLICANT: Boehringer, Reinier LH
/ APPLICANT: Woehl, Thorsten
/ APPLICANT: Boettger, Volker
/ TITLE OF INVENTION: Method of Producing Recombinant Antibodies
/ FILE REFERENCE: 2923-552
/ CURRENT APPLICATION NUMBER: US/10/635,908
/ CURRENT FILING DATE: 2003-08-07
/ PRIOR APPLICATION NUMBER: PCT/EP02/01283
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 60/327,008
/ PRIOR FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: 60/266,853
/ PRIOR FILING DATE: 2001-02-07
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn version 3.2
```

```
SEQ ID NO 5
/ LENGTH: 357
/ TYPE: DNA
/ ORGANISM: Artificial
/
/ FEATURE:
/ OTHER INFORMATION: mouse anti-human monoclonal antibody cDNA
/
US-10-635-908-5

Alignment Scores:
Pred. No.: 3,61e-76 Length: 357
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-635-908-6 (1-119) x US-10-635-908-5 (1-357)

QY 1 AspVallyLLeuValIGluserGlyGlyLeuValLlyLeuGlyGlySerLeuLysLeu 20
DB 1 GACGTGAAGCTGCTGAGCTGCGGGAGGCTTAGTGAAGCTTGAGAGGCTCCCTGAACCTC 60
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40
DB 61 TCCTGTGACGCTCTGAGATTCACTTCACTAATTAATGATGCTGGGTTGCGCAGACT 120
QY 41 ProGluLybArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60
DB 121 CCAGAGAAAGAGCTGAGAGTGTGCGACGCAATTAATGATGATGATGATACCTACTAT 180
QY 61 LeuAspThrValLlyGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTYr 80
DB 181 CTAGACACTGTGAAGGCGGATTCACATTTCAAGAGCAATGCCAAGAACCTCTGATC 240
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTYrCYsAlaArgHisArg 100
DB 241 CTGCAATGAGAGCTGAGAGTCTGAGACACAGCCTTGTTTTACTGTGCAAGACACCGC 300
QY 101 SerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 301 TCGGGCTACTTTTCTATGAGCTACTGGGGTCAAGAACTCAAGTACCGTCTCTCA 357

RESULT 3
US-10-333-235A-8
/ Sequence 8, Application US/10333235A
/ Publication No. US20040132007A1
/ GENERAL INFORMATION:
/ APPLICANT: COT-A-GENE AB
/ APPLICANT: Lelf, Lindholm
/ APPLICANT: Karin, Nord
/ APPLICANT: Pierre, Boulanger
/ APPLICANT: Rebecca, Gardner
/ TITLE OF INVENTION: Modified Virus
/ FILE REFERENCE: 9.7.72728/001
/ CURRENT APPLICATION NUMBER: US/10/333,235A
/ CURRENT FILING DATE: 2003-12-04
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 8
/ LENGTH: 1056
/ TYPE: DNA
/ ORGANISM: Artificial
/
/ FEATURE:
/ OTHER INFORMATION: G250 single chain antibody construct
/
US-10-333-235A-8

Alignment Scores:
Pred. No.: 1,69e-75 Length: 1056
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
```



US-10-635-908-6 (1-119) x US-10-333-235A-8 (1-1056)

```
QY 1 AspVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuLysLeu 20
DB 376 GACGTGAAGCTCGTGGAGTCTGGGGGAGCTTAGTGAAGCTTGAGAGGCTCCCTGAACATC 435
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyTrpMetSerTrpValArgGlnThr 40
DB 436 TCTGTGACGCTCTGGATTCACTTCAGTAACATATTAACATGCTTGGGTTGCCAGACT 495
QY 41 ProGluYsArgLeuGluLeuValAlaAlaAlaLeuSerAspGlyGlyIleThrTyTrp 60
DB 496 CCAGAGAAAGAGGCTGGAGTTGGTCGACGCAATTAATAGATGGTGTATCACTCTAT 555
QY 61 LeuAspThrVallyLeuGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyR 80
DB 556 CTAGACACCTGTGAAGGCGGATTCACCATTTCAAGAGACAAATGCCAAGAACACCTGTATC 615
QY 81 LeuGlnMetSerSerLeuLysSerGlyuAspThrAlaLeuPheTyrcyAlaArgHisArg 100
DB 616 CTGCATAATGACAGCTGTGAAGCTGAGGACACAGCCTTGTTTACTGTGCAAGACACCGC 675
QY 101 SerGlyTyTrpPheSerMetAspTyTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 676 TCGGGCTACTTTTCTATGACCTACTGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 732
```

## RESULT 4

```
US-10-333-235A-10
; Sequence 10, Application US/10333235A
; Publication No. US20040132007A1
; GENERAL INFORMATION:
; APPLICANT: GOF-A-GENE AB
; APPLICANT: Leif, Lindholm
; APPLICANT: Karin, Nord
; APPLICANT: Pierre, Boulanger
; APPLICANT: Rebecca, Gardner
; TITLE OF INVENTION: Modified Virus
; FILE REFERENCE: 9.7.72728/001
; CURRENT APPLICATION NUMBER: US/10/333,235A
; CURRENT FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fiber construct A1 G250
US-10-333-235A-10
```

Alignment Scores:

Pred. No.:	2.55e-75	Length:	1411
Score:	617.00	Matches:	119
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	8	Indels:	0
DB:	8	Gaps:	0

US-10-635-908-6 (1-119) x US-10-333-235A-10 (1-1411)

```
QY 1 AspVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuLysLeu 20
DB 722 GACGTGAAGCTCGTGGAGTCTGGGGGAGCTTAGTGAAGCTTGAGAGGCTCCCTGAACATC 781
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyTrpMetSerTrpValArgGlnThr 40
DB 782 TCTGTGACGCTCTGGATTCACTTCAGTAACATATTAACATGCTTGGGTTGCCAGACT 841
QY 41 ProGluYsArgLeuGluLeuValAlaAlaAlaLeuSerAspGlyGlyIleThrTyTrp 60
DB 842 CCAGAGAAAGAGGCTGGAGTTGGTCGACGCAATTAATAGATGGTGTATCACTCTAT 901
```

```
QY 61 LeuAspThrVallyLeuGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyR 80
DB 902 CTAGACACCTGTGAAGGCGGATTCACCATTTCAAGAGACAAATGCCAAGAACACCTGTATC 961
QY 81 LeuGlnMetSerSerLeuLysSerGlyuAspThrAlaLeuPheTyrcyAlaArgHisArg 100
DB 962 CTGCATAATGACAGCTGTGAAGCTGAGGACACAGCCTTGTTTACTGTGCAAGACACCGC 1021
QY 101 SerGlyTyTrpPheSerMetAspTyTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 1022 TCGGGCTACTTTTCTATGACCTACTGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 1078
```

## RESULT 5

```
US-10-333-235A-11
; Sequence 11, Application US/10333235A
; Publication No. US20040132007A1
; GENERAL INFORMATION:
; APPLICANT: GOF-A-GENE AB
; APPLICANT: Leif, Lindholm
; APPLICANT: Karin, Nord
; APPLICANT: Pierre, Boulanger
; APPLICANT: Rebecca, Gardner
; TITLE OF INVENTION: Modified Virus
; FILE REFERENCE: 9.7.72728/001
; CURRENT APPLICATION NUMBER: US/10/333,235A
; CURRENT FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 1702
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fiber construct A7 G250
US-10-333-235A-11
```

Alignment Scores:

Pred. No.:	3.34e-75	Length:	1702
Score:	617.00	Matches:	119
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	8	Indels:	0
DB:	8	Gaps:	0

US-10-635-908-6 (1-119) x US-10-333-235A-11 (1-1702)

```
QY 1 AspVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuLysLeu 20
DB 1013 GACGTGAAGCTCGTGGAGTCTGGGGGAGCTTAGTGAAGCTTGAGAGGCTCCCTGAACATC 1072
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyTrpMetSerTrpValArgGlnThr 40
DB 1073 TCTGTGACGCTCTGGATTCACTTCAGTAACATATTAACATGCTTGGGTTGCCAGACT 1132
QY 41 ProGluYsArgLeuGluLeuValAlaAlaAlaLeuSerAspGlyGlyIleThrTyTrp 60
DB 1133 CCAGAGAAAGAGGCTGGAGTTGGTCGACGCAATTAATAGTATGGTGTATCACTCTAT 1192
QY 61 LeuAspThrVallyLeuGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyR 80
DB 1193 CTAGACACCTGTGAAGGCGGATTCACCATTTCAAGAGACAAATGCCAAGAACACCTGTATC 1252
QY 81 LeuGlnMetSerSerLeuLysSerGlyuAspThrAlaLeuPheTyrcyAlaArgHisArg 100
DB 1253 CTGCATAATGACAGCTGTGAAGCTGAGGACACAGCCTTGTTTACTGTGCAAGACACCGC 1312
QY 101 SerGlyTyTrpPheSerMetAspTyTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 1313 TCGGGCTACTTTTCTATGACCTACTGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 1369
```

RESULT 6

US-10-635-908-9

; Sequence 9, Application US/10635908

/	NUMBER OF SEQ ID NOS:	56
/	SEQ ID NO 50	
/	LENGTH:	444
/	TYPE:	DNA
/	ORGANISM:	Mus musculus
/	FEATURE:	
/	OTHER INFORMATION:	murine G250 heavy chain variable region
/	US-10-504-389A-50	
 Alignment Scores:		
Pred. No.:	2,37e-74	Length: 444
Score:	605.00	Matches: 117
Percent Similarity:	96.3%	Conservative: 0
Best Local Similarity:	96.3%	Mismatches: 2
Query Match:	98.1%	Indels: 0
DB:	11	Gaps: 0
 US-10-635-908-6 (1-119) x US-10-504-389A-50 (1-444)		
QY	1 AspvallLLeuValGluSerGIyGLyIleuValLYLeuGIyGISerLeuLYLeu	20
Db	75 GAAGTAAAGCTGTGGAGCTGGGGACACTTAGTGGAAGCTTGAGGGTCCTGTAATC	134
QY	21 SerCyAlALASerGIyPhePhrPheSerAnTYrTYMetSertPvalArgJnThr	40
Db	135 TCGTGACGCCCTGGATTCACTTCAGTAACATTTTCATGTCCTTGGGTTCCGACA	194
QY	41 ProGUlyArGLeuGluleValAlaAlaleSenSarSpGIyIleThrTYrTYr	60
Db	195 CCAGAAGAGAGCTGGAGTTGGTCCAGACCATTATAATGATGGTGNATCACCTACT	254
QY	61 LeuAsPThtValLyGLyArPheThrIleSerArgAspAnaLYLeuThrLeuTYr	80
Db	255 CTAGACACGTGAAGGGCCGATTCCACATTCAGAGCAATGCAGAACACCCCTGAC	314
QY	81 LeuGIMetSerSerLeuLYSerGIuAsPThtAlaleuPheTYCYAlarGLieArg	100
Db	315 CTCGAATAGCAGCTGTGAAGCTGAGGACACAGCCCTGTTTACTGTGCAAGACACGC	374
QY	101 SerGIyTYrPheSerMetAsPTYTTPGLyngIyThrservalThrvAlSerSer	119
Db	375 TCAGGCTACTTTCATGACTGACTGAGGAGCAAGAACCTCATGACCGTCTCTCA	431
 RESULT 8		
US-10-226-795-31		
/	Sequence 31, Application US/10226795	
/	Publication No. US20040053865A1	
/	GENERAL INFORMATION:	
/	APPLICANT: HART, MARY KATE	
/	APPLICANT: WILSON, JULIE	
/	TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING	
/	TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN	
/	FILE REFERENCE: ARMY 166	
/	CURRENT APPLICATION NUMBER: US/10/226,795	
/	CURRENT FILING DATE: 2002-11-18	
/	NUMBER OF SEQ ID NOS: 40	
/	SOFTWARE: PatentIn Ver. 2.1	
/	SEQ ID NO 31	
/	LENGTH: 464	
/	TYPE: DNA	
/	ORGANISM: Artificial Sequence	
/	FEATURE:	
/	OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy	
/	OTHER INFORMATION: chain of Mab EGP13fe-1-2 DNA sequence	
/	US-10-226-795-31	
 Alignment Scores:		
Pred. No.:	2.72e-59	Length: 484
Score:	498.00	Matches: 98
Percent Similarity:	87.8%	Conservative: 10
Best Local Similarity:	79.7%	Mismatches: 11
Query Match:	80.7%	Indels: 4
DB:	8	Gaps: 1

US-10-635-908-6 (1-119) x US-10-226-795-31 (1-484)

```
QY 1 AspvallyleuValglusergIyglYleuVallyleuGllyserleuylsleu 20
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 GAAGTCAGAGCTGGAGTCTGGAGGAGGCTTAGTAGAAGCTGGAGGCTCCGAAATC 125
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgIntNr 40
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 TCCTGTGCAGCCTCTGGATTCGCTTCAGAGCTAGCATGTCTTGGGTTCCCGAGCT 185
QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyr 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 CCGAGAAAGAGGCTGGAGTGGTCCGATACATAGTCGTGTGGTTACCTACTAT 245
QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 246 CCAGACACTGTGAAGGCCGATTCACCATCTCCAGAGACAAATCCAAAGAACCTGTATC 305
QY 81 LeuGluMetSerSerleuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHis--- 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 CTGCAATGTAGAGCTGAGAGCTGAGAGACACAGCCATGTATTAAGTCTTCAAGACATATA 365
QY 100 -----ArgSerGlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThr 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 366 TATTACGGAGAGTGTCTATTCTATGCTATGACTGAGGCTCAAGGAACCTCAGTCACC 425
QY 117 ValSerSer 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 426 GTCTCTCTCA 434
```

## RESULT 9

```
US-09-881-823-11
: Sequence 11, Application US/09881823
: Patent No. US20020068066A1
: GENERAL INFORMATION:
: APPLICANT: SHI, WENYUAN
: APPLICANT: ANDERSON, MAXWELL
: APPLICANT: MORRISON, SHERIE
: APPLICANT: TRINH, RYAN
: APPLICANT: WIMS, LETITIA
: APPLICANT: CHEN, LI
: TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
: FILE REFERENCE: 22851-032
: CURRENT APPLICATION NUMBER: US/09/881,823
: CURRENT FILING DATE: 2001-06-15
: PRIOR APPLICATION NUMBER: US 07/378,577
: PRIOR FILING DATE: 1999-08-20
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 11
: LENGTH: 466
: TYPE: DNA
: ORGANISM: Murine
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (11)..(442)
US-09-881-823-11
```

## Alignment Scores:

```
Pred. No.: 6.8e-59 Length: 466
Score: 495.00 Matches: 98
Percent Similarity: 88.6% Conservative: 11
Best Local Similarity: 79.7% Mismatches: 10
Query Match: 80.2% Indels: 4
DB: 3 Gaps: 1
```

US-10-635-908-6 (1-119) x US-09-881-823-11 (1-466)

```
QY 1 AspvallyleuValglusergIyglYleuVallyleuGllyserleuylsleu 20
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 GACGTGAAGCTGGAGTCTGGAGGAGCTTAGTAGAACCTTGAGGAGTCTCCGAAACTC 127
```

```
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgIntNr 40
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 TCCTGTGCAGCCTCTGGATTCGCTTCAGAGCTAGCATGTCTTGGGTTCCCGAGCT 187
QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyr 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 CCGAGAAAGAGGCTGGAGTGGTCCGATTCATAGTAGTGTGTACTTACACTACTAT 247
QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 248 CCAGACAGTGAAGGCCGATTCACCATCTCCAGAGACAAATGCCAAAGAACCTGTATC 307
QY 81 LeuGluMetSerSerleuLysSerGluAspThrAlaLeuPheTyrCysAlaArg----- 98
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 CTGCAATGTAGCAGCTGAGAGCTGAGAGACACAGCCATGTATTAAGTCTTCAAGAGATGAC 367
QY 99 -----HisArgSerGlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThr 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 GGCTCTACGGCTCTATTACTATGCTATGACTACTGGGGTCAAGGAACCTCAGTCACC 427
QY 117 ValSerSer 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 428 GTCTCTCTCA 436
```

## RESULT 10

```
US-09-910-358D-5
: Sequence 5, Application US/0910358D
: Publication No. US20040052814A1
: GENERAL INFORMATION:
: APPLICANT: Shi, Wenyuan
: APPLICANT: Anderson, Maxwell
: APPLICANT: Morrison, Sherie
: APPLICANT: Trinh, Kham
: APPLICANT: Wims, Letitia
: APPLICANT: Chen, Li
: TITLE OF INVENTION: Fusion Proteins for Targeted Delivery of Antimicrobial Peptides
: FILE REFERENCE: 22851-033
: CURRENT APPLICATION NUMBER: US/09/910,358D
: CURRENT FILING DATE: 2001-07-19
: PRIOR APPLICATION NUMBER: US 09/378,577
: PRIOR FILING DATE: 1999-08-20
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 533
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthesized using sequential PCR techniques
: NAME/KEY: CDS
: LOCATION: (69)..(110)
: OTHER INFORMATION: Dvvar 1
: NAME/KEY: CDS
: LOCATION: (111)..(158)
: OTHER INFORMATION: Linker Peptide
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (159)..(533)
: OTHER INFORMATION: VH of SWLA3
US-09-910-358D-5
```

## Alignment Scores:

```
Pred. No.: 8.23e-59 Length: 533
Score: 495.00 Matches: 98
Percent Similarity: 88.6% Conservative: 11
Best Local Similarity: 79.7% Mismatches: 10
Query Match: 80.2% Indels: 4
DB: 3 Gaps: 1
```

US-10-635-908-6 (1-119) x US-09-910-358D-5 (1-533)

[illegible]

Qy	21	SeqCyValaAlaAsSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgInThr	40
Db	219	TCCTGTGAGGCTCTGGAATTCATCTTCAGTACCTATACCATGCTCTTGCGTCCAGACT	278
Qy	41	ProGluIysAspLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr	60
Db	279	CCGAGAAAGAGGCTGGAGTGGGTGGCATCTTAACTAGTGGGTACTTACACCTACTAT	338
Qy	61	LeuAspThrValIlylGlyIyrPheThrIleSerAlaAspAsnAllyAsnThrLeuTyr	80
Db	339	CCAGACAGATGGAAGGGCCGATTCACCATCCACAGACAAAGCCAAAGAACCCCTGAC	398
Qy	99	-----HisArgSerGlyTyrPheSerMetAspTyrTrpGlyGlyIlyThrSerValThr	116
Db	459	GGCTCCTACGGCTCCTATTACTATGACTATGACTCTAGGCGGTCAAGAACTCAGTACC	518
Qy	117	ValSerSer 119	
Db	519	GTCTCTTCA 527	
RESULT 12			
US-10-706-391-3			
Sequence 3, Application US/10706391			
Publication No. US20040137482A1			
GENERAL INFORMATION:			
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA			
APPLICANT: WASHINGTON DENTAL SERVICE			
APPLICANT: Eckert, Randal			
APPLICANT: Qi, Fengxia			
APPLICANT: Shi, Wenyuan			
APPLICANT: Anderson, Maxwell H.			
TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL			
FILE REFERENCE: 2101363-991600			
CURRENT APPLICATION NUMBER: US/10/706,391			
CURRENT FILING DATE: 2003-06-16			
PRIOR APPLICATION NUMBER: US 10/077,624			
PRIOR FILING DATE: 2002-02-14			
PRIOR APPLICATION NUMBER: US 09/910,358			
PRIOR FILING DATE: 2001-07-19			
PRIOR APPLICATION NUMBER: US 09/378,577			
PRIOR FILING DATE: 1999-08-20			
NUMBER OF SEQ ID NOS: 71			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 3			
LENGTH: 533			
TYPE: DNA			
ORGANISM: Artificial sequence			
FEATURE:			
OTHER INFORMATION: Synthesized using sequential PCR techniques			
US-10-706-391-3			
Alignment Scores:			
Pred. No.: 8,236-59 Length: 533			
Score: 495.00 Matches: 98			
Percent Similarity: 88.6% Conservative: 11			
Best Local Similarity: 79.7% Mismatches: 10			
Query Match: 80.2% Indels: 4			
DB: 8 Gaps: 1			
US-10-635-908-6 (1-119) x US-10-706-391-3 (1-533)			
Qy	1	AspValIlyLeuValGluSerGlyGlyIlyLeuValIlyLeuGlyGlySerLeuIlyLeu	20
Db	159	GACGTGAAGCTTGTGAGTCTGGGGGAGGCTTAGTGAAACCTGAGGGTCCCTGAAATC	218
Qy	21	SerCyValAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgInThr	40
Db	219	TCCTGTGAGGCTCTGGAATTCATCTTCAGTACCTATACCATGCTCTTGCGTCCAGACT	278

```
QY 41 ProGUlybArghleuValAlaAlaIleasnSerAspGlyGlyIleThrTYr 60
DB 279 CCGAGAAAGGCTGGAGTGGGTGCGATCCATTAGTGTGTGTTACTTACACTTACT 338
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTYr 80
DB 339 CCAGACAGGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACCCTGTAC 398
QY 81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTYrCysAlaArg----- 98
DB 399 CTGCAAAATGACCGAGTCTGGAAGTCTGAGACACAGCCCATGTATTACTGTTCAAGAGATGAC 458
QY 99 -----HisArgSerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThr 116
DB 459 GGCCTCAAGCGCTCTTACTTACTATGACTACTGGGCTCAAGAACCTCAGTAC 518
QY 117 ValSerSer 119
DB 519 GTCTCTTCA 527

RESULT 13
US-09-910-358D-1
; Sequence 1, Application US/09910358D
; Publication No. US20040052814A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Wenyan
; APPLICANT: Anderson, Maxwell
; APPLICANT: Morrison, Sherie
; APPLICANT: Trinh, Kham
; APPLICANT: Wims, Letitia
; APPLICANT: Chen, Li
; TITLE OF INVENTION: Fusion Proteins for Targeted Delivery of Antimicrobial Peptides
; FILE REFERENCE: 22851-033
; CURRENT APPLICATION NUMBER: US/09/910,358D
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized using sequential PCR techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)..(140)
; OTHER INFORMATION: Histatin 5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (141)..(188)
; OTHER INFORMATION: Linker Peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(563)
; OTHER INFORMATION: VH of SWLA3
US-09-910-358D-1

Alignment Scores:
Pred. No.: 8.9e-59 Length: 563
Score: 495.00 Matches: 98
Percent Similarity: 88.6% Conservative: 11
Best Local Similarity: 79.7% Mismatches: 10
Query Match: 80.2% Indels: 1
DB: 3 Gaps: 1

US-10-635-908-6 (1-119) x US-09-910-358D-1 (1-563)
QY 1 AspValIysLeuValGluSerGlyGlyGlyLeuValIysLeuGlyGlySerLeuIysLeu 20
DB 189 GACGTGAAGCTTGTGAGTCTGGGGAGCGCTTATGTAACCTCGAGGGTCCCTGAAACTC 248
```

```
QY 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40
DB 249 TCGTGACAGCCTTGAGATTCACTTCACTACTACTATACCATTGTTGGGTGCCAGACT 308
QY 41 ProGUlybArghleuValAlaAlaIleasnSerAspGlyGlyIleThrTYrTYr 60
DB 309 CCGAGAAAGGCTGGAGTGGGTGCGATCCATTAGTGTGTGTTACTTACACTTACT 368
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTYr 80
DB 369 CCAGACAGGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACCCTGTAC 428
QY 81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTYrCysAlaArg----- 98
DB 429 CTGCAAAATGACCGAGTCTGGAAGTCTGAGACACAGCCCATGTATTACTGTTCAAGAGATGAC 488
QY 99 -----HisArgSerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThr 116
DB 489 GGCCTCAAGCGCTCTTACTTACTATGACTACTGGGCTCAAGAACCTCAGTAC 548
QY 117 ValSerSer 119
DB 549 GTCTCTTCA 557

RESULT 14
US-10-077-624-1
; Sequence 1, Application US/10077624
; Publication No. US20030143234A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: WASHINGTON DENTAL SERVICE
; APPLICANT: Shi, Wenyan
; APPLICANT: Anderson, Maxwell
; APPLICANT: Morrison, Sherie
; APPLICANT: Trinh, Kham
; APPLICANT: Wims, Letitia
; APPLICANT: Chen, Li
; APPLICANT: Qi, Fengxia
; TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
; FILE REFERENCE: 2101363-991200
; CURRENT APPLICATION NUMBER: US/10/077,624
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 09/910,358
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized using sequential PCR techniques
US-10-077-624-1

Alignment Scores:
Pred. No.: 8.9e-59 Length: 563
Score: 495.00 Matches: 98
Percent Similarity: 88.6% Conservative: 11
Best Local Similarity: 79.7% Mismatches: 10
Query Match: 80.2% Indels: 4
DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-10-077-624-1 (1-563)
QY 1 AspValIysLeuValGluSerGlyGlyGlyLeuValIysLeuGlyGlySerLeuIysLeu 20
DB 189 GACGTGAAGCTTGTGAGTCTGGGGAGCGCTTATGTAACCTCGAGGGTCCCTGAAACTC 248
QY 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40
```

Db 249 TCCTGTCAGCCCTGCGATTCACTTCACTAGTATACCATGCTTGGGTGCGCAGACT 308  
Qy 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyr 60  
Db 309 CCGGAGAAAGGCTGAGTGGGTGCGCATCATTAAGTAGTGGTACTTACACTACTAT 368  
Qy 61 LeuAspThrValIleArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80  
Db 369 CCAGACAGGTGAGAGGCGCATCTCCAGACAAATGCCAAAGAACACCTGTATC 428  
Qy 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArg----- 98  
Db 429 CTGCAAAATGACCAAGTCTGAAGTCTGAGGACACAGCATATTAAGTCTTCAAGAGATGAC 488  
Qy 99 -----HisArgSerGlyTyrPheSerMetAspTyrTTPGlyGlnGlyThrSerValThr 116  
Db 489 GGCCTCTACGGCTCTATTACTATGACTATGACTACTGGGCTCAAGAACTCAGTCAACC 548  
Qy 117 ValSerSer 119  
Db 549 GTCTCTTCA 557

## RESULT 15

US-10-706-391-1  
; Sequence 1, Application US/10706391  
; Publication No. US20040137482A1  
; GENERAL INFORMATION:  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: WASHINGTON DENTAL SERVICE  
; APPLICANT: Eckert, Randall  
; APPLICANT: Qi, Fengxia  
; APPLICANT: Shi, Wenjuan  
; APPLICANT: Anderson, Maxwell H.  
; TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL  
; FILE REFERENCE: 2101363-991600  
; CURRENT APPLICATION NUMBER: US/10/706,391  
; CURRENT FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 10/077,624  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 09/910,358  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US 09/378,577  
; PRIOR FILING DATE: 1999-08-20  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 563  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized using sequential PCR techniques  
US-10-706-391-1

## Alignment Scores:

Pred. No.: 8.9e-59 Length: 563  
Score: 495.00 Matches: 98  
Percent Similarity: 88.6% Conservative: 11  
Best Local Similarity: 79.7% Mismatches: 10  
Query Match: 80.2% Indels: 4  
DB: 8 Gaps: 1

US-10-635-908-6 (1-119) x US-10-706-391-1 (1-563)

Qy 1 AspValIleLeuValGluSerGlyGlyGlyLeuValIleLeuGlyGlySerLeuLysLeu 20  
Db 189 GACGTAAAGCTTGTGAGTCTGGGGAGGCTTAGTGAACCTCGAGGGTCCCTGAAATC 248  
Qy 21 SerCysAlaIleSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40  
Db 249 TCCTGTCAGCCCTGCGATTCACTTCAAGTACTATACCATGCTTGGGTTCCGCGAGACT 308  
Qy 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60

Db 309 CCGGAGAAAGGCTGAGTGGGTGCGCATCATTAAGTAGTGGTACTTACACTACTAT 368  
Qy 61 LeuAspThrValIleArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80  
Db 369 CCAGACAGGTGAGAGGCGCATCTCCAGACAAATGCCAAAGAACACCTGTATC 428  
Qy 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArg----- 98  
Db 429 CTGCAAAATGACCAAGTCTGAAGTCTGAGGACACAGCATATTAAGTCTTCAAGAGATGAC 488  
Qy 99 -----HisArgSerGlyTyrPheSerMetAspTyrTTPGlyGlnGlyThrSerValThr 116  
Db 489 GGCCTCTACGGCTCTATTACTATGACTATGACTACTGGGCTCAAGAACTCAGTCAACC 548  
Qy 117 ValSerSer 119  
Db 549 GTCTCTTCA 557

Search completed: June 3, 2006, 07:32:36  
J0D time : 821.991 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 06:56:49 ; Search time 13.5796 Seconds  
(without alignments)  
1548.108 Million cell updates/sec

Title: US-10-635-908-6  
Perfect score: 617  
Sequence: 1 DVKLVSQGGGLVGLGSLKL.....RSGYFMDYQGTSTVVS 119

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 246837 seqs, 5886590 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+g2n.model -DEV=x1h  
-Q=/abs/BIOSWEB.spool/US10635908/runat\_02062006\_104226\_10433/app\_query.fasta.1  
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=trpbn -MINMATCH=0.1  
-LOPCU=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=abs05h  
-USR=US10635908 -OCG=1\_1\_26 -runat\_02062006\_104226\_10433 -NCPU=6 -ICPU=3  
-NO MMP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONCLOG -DEV -TIMEOUT=120  
-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:  
1: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US09\_NEW\_PUB.seq:  
2: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US06\_NEW\_PUB.seq:  
3: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US07\_NEW\_PUB.seq:  
4: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US08\_NEW\_PUB.seq:  
5: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10\_NEW\_PUB.seq:  
6: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11\_NEW\_PUB.seq:  
7: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US60\_NEW\_PUB.seq:  
8: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US60\_NEW\_PUB.seq:  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	476.5	77.2	1407	US-11-155-444-17	Sequence 17, Appl
2	452.5	73.3	2094	US-11-155-444-1	Sequence 1, Appl
3	452.5	73.3	2106	US-11-155-444-7	Sequence 1, Appl
4	452.5	73.3	2196	US-11-155-444-5	Sequence 5, Appl
5	452.5	73.3	2208	US-11-155-444-9	Sequence 9, Appl
6	440	71.3	873	US-11-154-103-27	Sequence 27, Appl
7	440	71.3	873	US-11-154-103-28	Sequence 28, Appl
8	437.5	70.9	870	US-11-154-103-30	Sequence 30, Appl
9	432	70.0	354	US-11-216-033-3	Sequence 3, Appl

10	431	69.9	357	7	US-11-300-563-23	Sequence 23, Appl
11	429.5	69.6	373	7	US-11-211-917-49	Sequence 49, Appl
12	429.5	69.6	373	7	US-11-211-917-95	Sequence 95, Appl
13	429.5	69.6	1410	7	US-11-211-917-53	Sequence 53, Appl
14	429	69.5	369	6	US-10-546-594-63	Sequence 63, Appl
15	429	69.5	369	6	US-10-546-594-69	Sequence 69, Appl
16	429	69.5	1419	6	US-10-546-594-129	Sequence 129, Appl
17	428.5	69.4	379	6	US-10-994-679-63	Sequence 63, Appl
18	427.5	69.3	362	7	US-11-023-959A-90	Sequence 90, Appl
19	425.5	69.0	366	7	US-11-254-679-37	Sequence 37, Appl
20	425	68.9	4027	7	US-11-169-140-1	Sequence 1, Appl
21	424.5	68.8	357	7	US-11-023-959A-185	Sequence 185, Appl
22	424	68.7	369	6	US-10-546-594-65	Sequence 65, Appl
23	423	68.6	732	6	US-10-503-433B-16	Sequence 16, Appl
24	423	68.6	803	6	US-10-503-433B-20	Sequence 20, Appl
25	422.5	68.5	345	7	US-11-023-959A-164	Sequence 164, Appl
26	422	68.4	351	7	US-11-254-679-65	Sequence 65, Appl
27	422	68.4	363	7	US-11-254-679-27	Sequence 27, Appl
28	422	68.4	801	6	US-10-503-433B-14	Sequence 14, Appl
29	421.5	68.3	357	7	US-11-023-959A-173	Sequence 173, Appl
30	421.5	68.3	360	7	US-11-254-679-8	Sequence 8, Appl
31	421	68.2	357	7	US-11-254-679-41	Sequence 41, Appl
32	419	67.9	741	7	US-11-216-033-5	Sequence 5, Appl
33	418	67.7	873	6	US-10-503-433B-19	Sequence 19, Appl
34	418	67.7	873	7	US-11-154-103-36	Sequence 36, Appl
35	417.5	67.7	357	7	US-11-023-959A-167	Sequence 167, Appl
36	417	67.6	706	6	US-11-254-679-61	Sequence 61, Appl
37	417	67.6	357	7	US-11-254-679-17	Sequence 17, Appl
38	416	67.6	764	6	US-10-503-433B-11	Sequence 11, Appl
39	416	67.4	357	7	US-11-254-679-45	Sequence 45, Appl
40	416	67.4	363	7	US-11-254-679-57	Sequence 57, Appl
41	416	67.4	369	7	US-11-254-679-12	Sequence 12, Appl
42	416	67.4	704	6	US-10-503-433B-15	Sequence 15, Appl
43	416	67.4	779	6	US-10-503-433B-18	Sequence 18, Appl
44	415.5	67.3	873	7	US-11-154-103-35	Sequence 35, Appl
45	415.5	67.3	360	7	US-11-254-679-16	Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-11-155-444-17  
Sequence 17, Application US/1155444  
Publication No. US20060104971A1  
GENERAL INFORMATION:  
APPLICANT: GABRIEL, ELLEN  
APPLICANT: BROWNING, JEFFREY L.  
TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND  
FILE REFERENCE: SIGNAL68CN  
CURRENT APPLICATION NUMBER: US/11/155,444  
CURRENT FILING DATE: 2005-06-17  
PRIOR APPLICATION NUMBER: PCT/US03/041393  
PRIOR FILING DATE: 2003-12-22  
PRIOR APPLICATION NUMBER: 60/435,154  
PRIOR FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: 60/435,185  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 17  
LENGTH: 1407  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: CBB1 pentameric  
OTHER INFORMATION: heavy chain antibody construct  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1404)  
US-11-155-444-17

## Alignment Scores:

Pred. No.: 2,65e-54 Length: 1407  
Score: 476.50 Matches: 92  
Percent Similarity: 85.8% Conservative: 11  
Best Local Similarity: 76.7% Mismatches: 16  
Query Match: 77.2% Indels: 1  
DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-155-444-17 (1-1407)

```
QY 1 AspValIysLeuValGluSerGlyGlyLeuValIysLeuGlySerLeuYsLeu 20
    1 GAGGTACAACGTGGTGAAGTCTGGGGAGGCTTAGGAAGCCTGGAGGGTCCCTGAGGCTC
DB 1 GAGGTACAACGTGGTGAAGTCTGGGGAGGCTTAGGAAGCCTGGAGGGTCCCTGAGGCTC 60
QY 21 SerCyAlaIaSerGlyPheThrPheSerAenTYrTYrMetSerTyrValArgGlnThr 40
    21 TCTGTGACGCTCTGGATTCACTTTCAGTACTATTACATGATGATTTGGTCCGACGACT
DB 61 TCTGTGACGCTCTGGATTCACTTTCAGTACTATTACATGATGATTTGGTCCGACGACT 120
QY 41 ProGluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60
    41 CCGGAAAAGAGGCTGAGTGGGTGGCAACCATTAAGTGTGTATTACCTACCTACTAT
DB 121 CCGGAAAAGAGGCTGAGTGGGTGGCAACCATTAAGTGTGTATTACCTACCTACTAT 180
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTYr 80
    61 CCAGACAGGTGAAGGGGCGATTCAACCATCTCCAGAGACAAATGCCAAGAACCTGTAC
DB 181 CCAGACAGGTGAAGGGGCGATTCAACCATCTCCAGAGACAAATGCCAAGAACCTGTAC 240
QY 81 LeuGlnMetSerSerLeuYsSerGluAspThrAlaLeuPheTYrCysAlaArgHisArg 100
    81 CTGCAATATGACGATCTGAGTCTGAGACACAGCCATGATATTAAGTGTAAAGAGAGAG
DB 241 CTGCAATATGACGATCTGAGTCTGAGACACAGCCATGATATTAAGTGTAAAGAGAGAG 300
QY 101 SerGly---TyrPheSerMetAspTYrTyrGlyGlnGlyThrSerValThrValSerSer 119
    101 AATGGTAACCTTTACTTACTTACTTACTGAGGCGCAAGGACCAAGGATCAGCTCTCTCA
DB 301 AATGGTAACCTTTACTTACTTACTTACTGAGGCGCAAGGACCAAGGATCAGCTCTCTCA 360
```

## RESULT 2

US-11-155-444-1  
Sequence 1, Application US/11155444  
Publication No. US20060104971A1  
GENERAL INFORMATION:  
APPLICANT: GARBER, ELLEN  
APPLICANT: BAILLY, VERNIQUE  
APPLICANT: BROWNING, JEFFREY L.  
TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND  
FILE REFERENCE: BGN168CN  
CURRENT APPLICATION NUMBER: US/11/155,444  
CURRENT FILING DATE: 2005-06-17  
PRIOR APPLICATION NUMBER: PCT/US03/041393  
PRIOR FILING DATE: 2003-12-22  
PRIOR APPLICATION NUMBER: 60/435,154  
PRIOR FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: 60/435,185  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patentin Ver. 3.3  
SEQ ID NO 1  
LENGTH: 2094  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of  
US-11-155-444-1  
OTHER INFORMATION: hucBE11/hubHA10 bispecific-1 antibody construct

## Alignment Scores:

Pred. No.: 7,23e-51 Length: 2094  
Score: 452.50 Matches: 87  
Percent Similarity: 85.0% Conservative: 15  
Best Local Similarity: 72.5% Mismatches: 17  
Query Match: 73.3% Indels: 1  
DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-155-444-1 (1-2094)

```
QY 1 AspValIysLeuValGluSerGlyGlyLeuValIysLeuGlySerLeuYsLeu 20
    1 GAGGTACAACGTGGTGAAGTCTGGGGAGGCTTAGGAAGCCTGGAGGGTCCCTGAGGCTC
DB 1 GAGGTACAACGTGGTGAAGTCTGGGGAGGCTTAGGAAGCCTGGAGGGTCCCTGAGGCTC 60
QY 21 SerCyAlaIaSerGlyPheThrPheSerAenTYrTYrMetSerTyrValArgGlnThr 40
    21 TCTGTGACGCTCTGGATTCACTTTCAGTACTATTACATGATGATTTGGTCCGACGCTC
DB 61 TCTGTGACGCTCTGGATTCACTTTCAGTACTATTACATGATGATTTGGTCCGACGCTC 120
QY 41 ProGluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60
    41 CCGGAAAAGAGGCTGAGTGGGTGGCAACCATTAAGTGTGTATTACCTGCGCAAGAGAGAG
DB 121 CCGGAAAAGAGGCTGAGTGGGTGGCAACCATTAAGTGTGTATTACCTGCGCAAGAGAGAG 180
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTYr 80
    61 CCAGACAGGTGAAGGGGCGATTCAACCATCTCCAGAGACAAATGCCAAGAACCTGTAC
DB 181 CCAGACAGGTGAAGGGGCGATTCAACCATCTCCAGAGACAAATGCCAAGAACCTGTAC 240
QY 81 LeuGlnMetSerSerLeuYsSerGluAspThrAlaLeuPheTYrCysAlaArgHisArg 100
    81 CTGCAATATGACGATCTGAGTCTGAGACACAGCCATGATATTAAGTGTAAAGAGAGAG
DB 241 CTGCAATATGACGATCTGAGTCTGAGACACAGCCATGATATTAAGTGTAAAGAGAGAG 300
QY 101 SerGly---TyrPheSerMetAspTYrTyrGlyGlnGlyThrSerValThrValSerSer 119
    101 AATGGTAACCTTTACTTACTTACTTACTGAGGCGCAAGGACCAAGGATCAGCTCTCTCA
DB 301 AATGGTAACCTTTACTTACTTACTTACTGAGGCGCAAGGACCAAGGATCAGCTCTCTCA 360
```

## RESULT 3

US-11-155-444-7  
Sequence 7, Application US/11155444  
Publication No. US20060104971A1  
GENERAL INFORMATION:  
APPLICANT: GARBER, ELLEN  
APPLICANT: BAILLY, VERNIQUE  
APPLICANT: BROWNING, JEFFREY L.  
TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND  
FILE REFERENCE: BGN168CN  
CURRENT APPLICATION NUMBER: US/11/155,444  
CURRENT FILING DATE: 2005-06-17  
PRIOR APPLICATION NUMBER: PCT/US03/041393  
PRIOR FILING DATE: 2003-12-22  
PRIOR APPLICATION NUMBER: 60/435,154  
PRIOR FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: 60/435,185  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patentin Ver. 3.3  
SEQ ID NO 7  
LENGTH: 2106  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of  
US-11-155-444-7  
OTHER INFORMATION: hucBE11 monospecific-1 antibody construct

## Alignment Scores:

Pred. No.: 7,29e-51 Length: 2106  
Score: 452.50 Matches: 87  
Percent Similarity: 85.0% Conservative: 15  
Best Local Similarity: 72.5% Mismatches: 17  
Query Match: 73.3% Indels: 1  
DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-155-444-7 (1-2106)

```
QY 1 AspValIysLeuValGluSerGlyGlyLeuValIysLeuGlySerLeuYsLeu 20
    1 GAGGTACAACGTGGTGAAGTCTGGGGAGGCTTAGGAAGCCTGGAGGGTCCCTGAGGCTC
DB 1 GAGGTACAACGTGGTGAAGTCTGGGGAGGCTTAGGAAGCCTGGAGGGTCCCTGAGGCTC 60
QY 21 SerCyAlaIaSerGlyPheThrPheSerAenTYrTYrMetSerTyrValArgGlnThr 40
    21 TCTGTGACGCTCTGGATTCACTTTCAGTACTATTACATGATGATTTGGTCCGACGCTC
DB 61 TCTGTGACGCTCTGGATTCACTTTCAGTACTATTACATGATGATTTGGTCCGACGCTC 120
```



```
QY 41 ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyr 60
|||
DB 121 CCGGGAAGAGGGGCTGAGTGGGTGCGAACCATTAAGTGGTGGTATTACACTACTAT 180
|||
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80
|||
DB 181 CCAGACAGTGTGAAGGGCGCATTCACCATCTCCAGAGACAAATGCCAAGAACGCTCTTAC 240
|||
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
|||
DB 241 CTGCAATGAGCAGCTGAGGGCTGAGAGACAGCTGTGATTACTGCCAAGAGAGAG 300
|||
QY 101 SerGly---TyrPheSerMetAspTyrTyrGlyGlnGlyThrSerValThrValSerSer 119
|||
DB 301 AATGGTAACCTTTACTTACTTACTTACTTACTGAGGCGCAAGGAGCAGCGTACCGTCTCTCA 360
|||
RESULT 4
US-11-155-444-5
; Sequence 5, Application US/11155444
; Publication No. US20060104971A1
; GENERAL INFORMATION:
; APPLICANT: GARBER, ELLEN
; APPLICANT: BAILLY, VERONIQUE
; APPLICANT: BROWNING, JEFFREY L.
; TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: BGN168CN
; CURRENT APPLICATION NUMBER: US/11/155,444
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/US03/041393
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: 60/435,154
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/435,185
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: huCBEL1/huBHA10
; OTHER INFORMATION: bispecific-2 antibody construct
US-11-155-444-5

Alignment Scores:
Pred. No.: 7,73e-51 Length: 2196
Score: 452.50 Matches: 87
Percent Similarity: 85.0% Conservative: 15
Best Local Similarity: 72.5% Mismatches: 17
Query Match: 73.3% Indels: 1
DB: Gaps: 1

US-10-635-908-6 (1-119) x US-11-155-444-5 (1-2196)
QY 1 AspValIysLeuValGluSerGlyGlyLeuValIysLeuGlyGlySerLeuLysLeu 20
|||
DB 1 GAGGTACAACTGGTGGAGTCTGGGGAGGCTTAAGTAAGCTTGAGGGTCCCTGAGGCTC 60
|||
QY 21 SerCysAlaIasSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
|||
DB 61 TCCGTGAGGCTCTGGATTCACCTTTCAGTACTATTACATGATTTGGTTTCGCAGGCC 120
|||
QY 41 ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
|||
DB 121 CCGGGAAGAGGGCTGAGTGGGTGCGCAACCATTAAGTGGTGGTATTACACTACTAT 180
|||
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80
|||
DB 181 CCAGACAGTGTGAAGGGCGCATTCACCATCTCCAGAGACAAATGCCAAGAACGCTCTAC 240
|||
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
|||
DB 101 SerGly---TyrPheSerMetAspTyrTyrGlyGlnGlyThrSerValThrValSerSer 119
|||
DB 301 AATGGTAACCTTTACTTACTTACTTACTTACTGAGGCGCAAGGAGCAGCGTACCGTCTCTCA 360
|||
RESULT 5
US-11-155-444-9
; Sequence 9, Application US/11155444
; Publication No. US20060104971A1
; GENERAL INFORMATION:
; APPLICANT: GARBER, ELLEN
; APPLICANT: BAILLY, VERONIQUE
; APPLICANT: BROWNING, JEFFREY L.
; TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: BGN168CN
; CURRENT APPLICATION NUMBER: US/11/155,444
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/US03/041393
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: 60/435,154
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/435,185
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 9
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: huCBEL1 monospecific-2
; OTHER INFORMATION: antibody construct
US-11-155-444-9

Alignment Scores:
Pred. No.: 7,79e-51 Length: 2208
Score: 452.50 Matches: 87
Percent Similarity: 85.0% Conservative: 15
Best Local Similarity: 72.5% Mismatches: 17
Query Match: 73.3% Indels: 1
DB: Gaps: 1

US-10-635-908-6 (1-119) x US-11-155-444-9 (1-2208)
QY 1 AspValIysLeuValGluSerGlyGlyLeuValIysLeuGlyGlySerLeuLysLeu 20
|||
DB 1 GAGGTACAACTGGTGGAGTCTGGGGAGGCTTAAGTAAGCTTGAGGGTCCCTGAGGCTC 60
|||
QY 21 SerCysAlaIasSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
|||
DB 61 TCCGTGAGGCTCTGGATTCACCTTTCAGTACTATTACATGATTTGGTTTCGCAGGCC 120
|||
QY 41 ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
|||
DB 121 CCGGGAAGAGGGCTGAGTGGGTGCGCAACCATTAAGTGGTGGTATTACACTACTAT 180
|||
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80
|||
DB 181 CCAGACAGTGTGAAGGGCGCATTCACCATCTCCAGAGACAAATGCCAAGAACGCTCTAC 240
|||
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
|||
DB 241 CTGCAATGAGCAGCTGAGGGCTGAGAGACAGCTGTGATTACTGCCAAGAGAGAG 300
|||
QY 101 SerGly---TyrPheSerMetAspTyrTyrGlyGlnGlyThrSerValThrValSerSer 119
|||
DB 301 AATGGTAACCTTTACTTACTTACTTACTTACTGAGGCGCAAGGAGCAGCGTACCGTCTCTCA 360
|||
RESULT 6
US-11-154-103-27
```

```
/ Sequence 27, Application US/11154103
/ Publication No. US2006009205A1
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, GREGORY P.
/ APPLICANT: HORAK, EVA M.
/ APPLICANT: WEINER, LOUIS M.
/ APPLICANT: JAMES, MARKS D.
/ TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
/ FILE REFERENCE: 407T-000420US
/ CURRENT APPLICATION NUMBER: US/11/154,103
/ PRIOR FILING DATE: 2005-06-15
/ PRIOR APPLICATION NUMBER: US 60/370,276
/ PRIOR FILING DATE: 2002-04-02
/ PRIOR APPLICATION NUMBER: US10/406,830
/ PRIOR FILING DATE: 2003-04-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 27
/ LENGTH: 873
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-11-154-103-27

Alignment Scores:
Pred. No.: 9,856-50 Length: 873
Score: 440.00 Matches: 85
Percent Similarity: 84.7% Conservative: 15
Best Local Similarity: 72.0% Mismatches: 18
Query Match: 71.3% Indels: 0
Gaps: 0
DB: 7

US-10-635-908-6 (1-119) x US-11-154-103-27 (1-873)

QY 2 ValLyLeuValGluSerGlyGlyValLeuValLeuGlyGlySerLeuLeuSer 21
DB 70 GTGCACTGGTGAAGCTGGGGAGGCTGTGACAGCCTGGGGGCTCCGAGACTCTCC 129
QY 22 CysAlaIAsersGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThrPro 41
DB 130 TGTGACGCTCTGAGATTACCTTCCGACGTATGCCATGAGCTGGGTCGGCAGGCTCCA 189
QY 42 GluLyArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYrLeu 61
DB 190 GGGAAAGGGGCTGAGTGGGCTCAGCTATTAGTGTGCTGATTAACAATCTACGCA 249
QY 62 AspThrVallyLeuGlyArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuLeu 81
DB 250 GACTCCGTGAAGGCGGCTGACCATCTCCAGAGCAATTCAGAGAACGCTGTATCTG 309
QY 82 GlnMetSerSerLeuLeuSerGluAspThrAlaLeuPheTYrCysAlaArgHisArgSer 101
DB 310 CAATGAACAGCTGAGAGCGGACGACACGGCGCTTATTACTGTGCAAAATGACAAAGT 369
QY 102 GlyTYrPheSerMetAspTYrTrpGlyGlnGlyIleThrSerValThrValSerSer 119
DB 370 AACGCGTTCGACTTGACTACTGGGGCCAGGAAACCTGTGTCACGCTCTCTCA 423

RESULT 7
US-11-154-103-28
/ Sequence 28, Application US/11154103
/ Publication No. US2006009205A1
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, GREGORY P.
/ APPLICANT: HORAK, EVA M.
/ APPLICANT: WEINER, LOUIS M.
/ APPLICANT: JAMES, MARKS D.
/ TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
/ FILE REFERENCE: 407T-000420US
/ CURRENT APPLICATION NUMBER: US/11/154,103
```

```
/ CURRENT FILING DATE: 2005-06-15
/ PRIOR APPLICATION NUMBER: US 60/370,276
/ PRIOR FILING DATE: 2002-04-02
/ PRIOR APPLICATION NUMBER: US10/406,830
/ PRIOR FILING DATE: 2003-04-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 28
/ LENGTH: 873
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-11-154-103-28

Alignment Scores:
Pred. No.: 9,856-50 Length: 873
Score: 440.00 Matches: 85
Percent Similarity: 84.7% Conservative: 15
Best Local Similarity: 72.0% Mismatches: 18
Query Match: 71.3% Indels: 0
Gaps: 0
DB: 7

US-10-635-908-6 (1-119) x US-11-154-103-28 (1-873)

QY 2 ValLyLeuValGluSerGlyGlyValLeuValLeuGlyGlySerLeuLeuSer 21
DB 70 GTGCACTGGTGAAGCTGGGGAGGCTGTGACAGCCTGGGGGCTCCGAGACTCTCC 129
QY 22 CysAlaIAsersGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThrPro 41
DB 130 TGTGACGCTCTGAGATTACCTTCCGACGTATGCCATGAGCTGGGTCGGCAGGCTCCA 189
QY 42 GluLyArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYrLeu 61
DB 190 GGGAAAGGGGCTGAGTGGGCTCAGCTATTAGTGTGCTGATTAACAATCTACGCA 249
QY 62 AspThrVallyLeuGlyArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuLeu 81
DB 250 GACTCCGTGAAGGCGGCTGACCATCTCCAGAGCAATTCAGAGAACGCTGTATCTG 309
QY 82 GlnMetSerSerLeuLeuSerGluAspThrAlaLeuPheTYrCysAlaArgHisArgSer 101
DB 310 CAATGAACAGCTGAGAGCGGACGACACGGCGCTTATTACTGTGCAAAATGACAAAGT 369
QY 102 GlyTYrPheSerMetAspTYrTrpGlyGlnGlyIleThrSerValThrValSerSer 119
DB 370 AACGCGTTCGACTTGACTACTGGGGCCAGGAAACCTGTGTCACGCTCTCTCA 423

RESULT 8
US-11-154-103-30
/ Sequence 30, Application US/11154103
/ Publication No. US2006009205A1
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, GREGORY P.
/ APPLICANT: HORAK, EVA M.
/ APPLICANT: WEINER, LOUIS M.
/ APPLICANT: JAMES, MARKS D.
/ TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
/ FILE REFERENCE: 407T-000420US
/ CURRENT APPLICATION NUMBER: US/11/154,103
/ CURRENT FILING DATE: 2005-06-15
/ PRIOR APPLICATION NUMBER: US 60/370,276
/ PRIOR FILING DATE: 2002-04-02
/ PRIOR APPLICATION NUMBER: US10/406,830
/ PRIOR FILING DATE: 2003-04-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 30
/ LENGTH: 870
/ TYPE: DNA
/ ORGANISM: Artificial
```

FEATURE:  
OTHER INFORMATION: Nucleic acid encoding single chain antibody.  
US-11-154-103-30

Alignment Scores:  
Pred. No.: 2,11e-49 Length: 870  
Score: 437.50 Matches: 87  
Percent Similarity: 85.7% Conservative: 15  
Best Local Similarity: 73.1% Mismatches: 14  
Query Match: 70.9% Indels: 3  
DB: 7 Gaps: 2

US-10-635-908-6 (1-119) x US-11-154-103-30 (1-870)

QY 2 VALLVLEUVALGLUSERGLVGLYGLYLEUVALVLEUGLVGLYSERLEULYSLEUSER 21  
DB GTGCAGCTCGAGAGTGGGGGAGGCTTGTCAAGCTGGGGGTCCTGAGACTCTCC 129  
QY 22 CYAALASERGLYPHERPHERSERANTYRTYRMESERTYVALARGINTHPRPO 41  
DB TGTGCAGCTCGAGAGTGGGGGAGGCTTGTCAAGCTGGGGGTCCTGAGACTCTCC 189  
QY 42 GLULYARGLEUGLULEUVALAALALEASERASPGVGLYILETHRTYRTYLEU 61  
DB GGAAAGGGCTGAGTGGGTGCGCCACATTAACCGCATGGAAGTGCACCTTATATGTG 249  
QY 62 ASPTHVALLYGLYARGPHERTHLLESERARGASPSANALALYSANTHRLTYRLEU 81  
DB GACTCTGTGAAGGCGCATTCACCATCTCCAGAGACACCCCAAGAACTCAGTATCTG 309  
QY 82 GLMERSESERLEULYSERGLUASPTHRALALEUPHERTYCYAALARGHSARGSER 101  
DB 310 CAATGACACGCTGAGAGCGGAGACACCGCTGTGTATTAAGTGTGAGAGATCGGGC 369  
QY 102 ---GLYTRPHERSERMETAPTYRTTGLYGLNGLYTHSERVALTHRLSER 119  
DB 370 GTGGGAGTCTTC-----GATCTCTGGGGCGTGGGACCTGTGACCGTCTCTCA 420

RESULT 9  
US-11-216-033-3  
Sequence 3, Application US/11216033  
Publication No. US20060104899A1  
GENERAL INFORMATION:

APPLICANT: HANSEN, HANS J.  
APPLICANT: GRIFETHS, GARY L.  
APPLICANT: MCBRIDE, WILLIAM J.  
APPLICANT: LEUNG, SHUI-ON  
APPLICANT: QU, ZHENGXING  
TITLE OF INVENTION: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR  
FILE REFERENCE: 40923-0074USA  
CURRENT APPLICATION NUMBER: US/11/216,033  
CURRENT FILING DATE: 2005-09-01  
PRIOR APPLICATION NUMBER: US/09/823,746  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 09/337,756  
PRIOR FILING DATE: 1999-06-22  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 3  
LENGTH: 354  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(354)  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic 679 Vh  
US-11-216-033-3

Alignment Scores:  
Pred. No.: 3.25e-49 Length: 354

Score: 432.00 Matches: 86  
Percent Similarity: 82.2% Conservative: 11  
Best Local Similarity: 72.9% Mismatches: 21  
Query Match: 70.0% Indels: 0  
DB: 7 Gaps: 0

US-10-635-908-6 (1-119) x US-11-216-033-3 (1-354)

QY 2 VALLVLEUVALGLUSERGLVGLYGLYLEUVALVLEUGLVGLYSERLEULYSLEUSER 21  
DB GTGCAGCTCGAGAGTGGGGGAGGCTTGTCAAGCTGGGGGTCCTGAGACTCTCC 60  
QY 22 CYAALASERGLYPHERPHERSERANTYRTYRMESERTYVALARGINTHPRPO 41  
DB TGTGCAGCTCGAGAGTGGGGGAGGCTTGTCAAGCTGGGGGTCCTGAGACTCTCC 120  
QY 42 GLULYARGLEUGLULEUVALAALALEASERASPGVGLYILETHRTYRTYLEU 61  
DB GGAAAGGGCTGAGTGGGTGCGCCACATTAACCGCATGGAAGTGCACCTTATATGTG 180  
QY 62 ASPTHVALLYGLYARGPHERTHLLESERARGASPSANALALYSANTHRLTYRLEU 81  
DB GACAGTGTGAAGGCTGAGTTCACCATCTCCAGAGACAAATGCCAAGAACTATATCTG 240  
QY 82 GLMERSESERLEULYSERGLUASPTHRALALEUPHERTYCYAALARGHSARGSER 101  
DB 241 CAATGACACGCTGAGAGCGGAGACACCGCTGTGTATTAAGTGTGAGAGATCGGGC 300  
QY 102 GLYTRPHERSERMETAPTYRTTGLYGLNGLYTHSERVALTHRLSER 119  
DB 301 GGGGACTGGGACTTCATGCTCTGGGGCCAGGACCAACGCTCTCCTCTCA 354

RESULT 10  
US-11-300-563-23

Sequence 23, Application US/11300563  
Publication No. US20060088526A1  
GENERAL INFORMATION:  
APPLICANT: BOLT, SARAH L.  
APPLICANT: CLARK, MICHAEL R.  
APPLICANT: GORMAN, SCOTT D.  
APPLICANT: ROUTLEDGE, EDWARD G.  
APPLICANT: WALDMANN, HERMAN  
TITLE OF INVENTION: HUMANIZED ANTI-CD3 SPECIFIC ANTIBODIES (AS AMENDED)  
FILE REFERENCE: 604-704  
CURRENT APPLICATION NUMBER: US/11/300,563  
CURRENT FILING DATE: 2005-12-15  
PRIOR APPLICATION NUMBER: 10/743,423  
PRIOR FILING DATE: 2003-12-23  
PRIOR APPLICATION NUMBER: 08/478,684  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 9206422.9  
PRIOR FILING DATE: 1992-03-24  
PRIOR APPLICATION NUMBER: PCT/GB92/01933  
PRIOR FILING DATE: 1992-10-21  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 23  
LENGTH: 357  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic nucleotide  
US-11-300-563-23

Alignment Scores:  
Pred. No.: 4.47e-49 Length: 357  
Score: 431.00 Matches: 82  
Percent Similarity: 84.9% Conservative: 19  
Best Local Similarity: 68.9% Mismatches: 18  
Query Match: 69.9% Indels: 0  
DB: 7 Gaps: 0

US-10-635-908-6 (1-119) x US-11-300-563-23 (1-357)

QY 1 AspVallyLeuValGluSerGlyGlyGlyLeuValLeuGlyGlySerLeuYsLeu 20  
Db 1 GAGGTCCAACTGCTGGAGTCTGGGGCGGCTTTAGTGCACAGCTGGAGGGTCCCTGAGACTC 60

QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40  
Db 61 TCTGTGGCAGCTCAGAGATTCACTTCCAGTAGCTTCCAAATGGCCGGGTCCGCGAGGCT 120

QY 41 ProGluYArgLeuGluLeuValAlaAlaLeuSerAspGlyGlyIleThrTYrTYr 60  
Db 121 CAGGGAAGGCTGTGAGTGGGTCTCAACCACTTACAGTGTGTGTGAAGTACTTACT 180

QY 61 LeuAspThrVallyGlyArgPheThrIleSerAspAspAlaAlaYsAsnThrLeuTYr 80  
Db 181 CGAGACTCCGTGAAGGGCGGATTCACCTATCTCAGAGATAATGAAAATACCTATAC 240

QY 81 LeuGlnMetSerSerLeuYsSerGlyuAspThrAlaLeuPheTYrCYeAlaArgHisArg 100  
Db 241 CTGCCAATGAATAGTCTGAGGGCTGAGACACGGCGCTTATTACTGTCCAAATTTTCG 300

QY 101 SerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThrValSerSer 119  
Db 301 CAGTACAGTGGTGGCTTTGATTACTGGGGCCAAAGGACCTGTCTCAGCTTCTCTCA 357

RESULT 11

US-11-211-917-49

/ Sequence 49, Application US/11211917

/ Publication No. US20060093600A1

/ GENERAL INFORMATION:

/ APPLICANT: BEDIAN, VAHE

/ APPLICANT: GLADUE, RONALD P.

/ APPLICANT: CORVALAN, JOSE

/ APPLICANT: JIA, XIAO-CHI

/ APPLICANT: FENG, XIAO

/ TITLE OF INVENTION: ANTIBODIES TO CD40

/ FILE REFERENCE: ABX-PF/3 US

/ CURRENT APPLICATION NUMBER: US/11/211,917

/ PRIOR FILING DATE: 2005-08-25

/ PRIOR APPLICATION NUMBER: US/10/292,088

/ PRIOR FILING DATE: 2002-11-08

/ PRIOR APPLICATION NUMBER: 60/348,980

/ PRIOR FILING DATE: 2001-11-09

/ NUMBER OF SEQ ID NOS: 147

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 49

/ LENGTH: 373

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-11-211-917-49

Alignment Scores:

Pred. No.: 7.52e-49 Length: 373

Score: 429.50 Matches: 85

Percent Similarity: 80.5% Conservative: 14

Best Local Similarity: 69.1% Mismatches: 19

Query Match: 69.6% Indels: 5

DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-211-917-49 (1-373)

QY 2 VallyLeuValGluSerGlyGlyGlyLeuValLeuGlyGlySerLeuYsLeuSer 21  
Db 4 GTGCACCTGGTGAAGTCTGGGGAGGCGTGTCCAGCTGCAGGCTCCCTGAGACTCTCC 63

QY 22 CyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThrPro 41  
Db 64 TGTGACGCTGTGATTCACCTTCAAGTCCGTATGGCAGCTGGGGCCGCGAGGCTCCA 123

QY 42 GluLYArgLeuGluLeuValAlaAlaLeuSerAspGlyGlyIleThrTYrTYrLeu 61  
Db 124 GCGAAGGGGCTGAGAGTGGGTGAGCTTATCATCTGATGAGGTAAATAATCTATGCC 183

QY 62 AspThrVallyGlyArgPheThrIleSerArgAspAlaAlaYsAsnThrLeuTYrLeu 81  
Db 184 GACTCCGGGAAGGGCGGATTCCACATCTCCAGAGCAATTCMAAAGCGCTGATCTG 243

QY 82 GlnMetSerSerLeuYsSerGlyuAspThrAlaLeuPheTYrCYeAlaArgHisArgSer 101  
Db 244 CAAATGAACAGCTGAGAGCTGAGGACAGGCTGTGTATTACTGTACAGAGAGAGGACT 303

QY 102 Gly-----TYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThr 116  
Db 304 GGAAGACTTACTACCACTACTGTGTATGACGCTGGGGCCAAAGGACACAGCTCAC 363

QY 117 ValSerSer 119  
Db 364 GTCTCTCCA 372

RESULT 12

US-11-211-917-95

/ Sequence 95, Application US/11211917

/ Publication No. US20060093600A1

/ GENERAL INFORMATION:

/ APPLICANT: BEDIAN, VAHE

/ APPLICANT: GLADUE, RONALD P.

/ APPLICANT: CORVALAN, JOSE

/ APPLICANT: JIA, XIAO-CHI

/ APPLICANT: FENG, XIAO

/ TITLE OF INVENTION: ANTIBODIES TO CD40

/ FILE REFERENCE: ABX-PF/3 US

/ CURRENT APPLICATION NUMBER: US/11/211,917

/ PRIOR FILING DATE: 2005-08-25

/ PRIOR APPLICATION NUMBER: US/10/292,088

/ PRIOR FILING DATE: 2002-11-08

/ PRIOR APPLICATION NUMBER: 60/348,980

/ PRIOR FILING DATE: 2001-11-09

/ NUMBER OF SEQ ID NOS: 147

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 95

/ LENGTH: 373

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-11-211-917-95

Alignment Scores:

Pred. No.: 7.52e-49 Length: 373

Score: 429.50 Matches: 85

Percent Similarity: 80.5% Conservative: 14

Best Local Similarity: 69.1% Mismatches: 19

Query Match: 69.6% Indels: 5

DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-211-917-95 (1-373)

QY 2 VallyLeuValGluSerGlyGlyGlyLeuValLeuGlyGlySerLeuYsLeuSer 21  
Db 4 GTGCACCTGGTGAAGTCTGGGGAGGCGTGTCCAGCTGCAGGAGTCCCTGAGACTCTCC 63

QY 22 CyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThrPro 41  
Db 64 TGTGACGCTGTGATTCACCTTCAAGTCCGTATGGCAGCTGGGGCCGCGAGGCTCCA 123

QY 42 GluLYArgLeuGluLeuValAlaAlaLeuSerAspGlyGlyIleThrTYrTYrLeu 61  
Db 124 GCGAAGGGGCTGAGAGTGGGTGAGCTTATCATCTGATGAGGTAAATAATCTATGCC 183

QY 62 AspThrVallyGlyArgPheThrIleSerArgAspAlaAlaYsAsnThrLeuTYrLeu 81  
Db 184 GACTCCGTGAAGGGCGGATTCCACATCTCCAGAGCAATTCMAAAGCGCTGATCTG 243

QY 82 GlnMetSerSerLeuYsSerGlyuAspThrAlaLeuPheTYrCYeAlaArgHisArgSer 101  
Db 244 CAAATGAACAGCTGAGAGCTGAGGACAGGCTGTGTATTACTGTACAGAGAGGAGACT 303



```
; Sequence 69, Application US/10546594
; Publication No. US2006008538A1
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: AOKI, Masahiko
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITAMI, Seima
; APPLICANT: UMEKI, Hiroe
; APPLICANT: SAIKAWA, Yoshiro
; APPLICANT: KUMAI, Koichiro
; APPLICANT: FUKUDA, Kazumasa
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND GENE ENCODING THE SAME, HYBRIDOMA, PHARMA
; FILE REFERENCE: 238067
; CURRENT APPLICATION NUMBER: US/10/546,594
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: JP 2003/54670
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: JP 2003/194643
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 69
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(369)
; OTHER INFORMATION:
US-10-546-594-69
```

```
Alignment Scores:
Pred. No.: 8.63e-49 Length: 369
Score: 429.00 Matches: 85
Percent Similarity: 81.3% Conservative: 15
Best Local Similarity: 69.1% Mismatches: 19
Query Match: 69.5% Indels: 4
DB: Gaps: 1
```

US-10-635-908-6 (1-119) x US-10-546-594-69 (1-369)

```
QY 1 AspValLysLeuValLysSerGlyGlyValLysLeuGlySerLeuLysLeu 20
DB 1 GAGGTGACCTGCTGGAGCTGGGAGGCTGAGCTGAGCTGAGCTGAGCTG 60
QY 21 SerCysAlaIleSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
DB 61 TCCTGTGACGCTCTGATTCACCTTCAGTACGCTATGCTACGCTGCGCCAGGCT 120
QY 41 ProGluLysArgLeuLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
DB 121 CCAGGCAAGGGCTGGAGTGGGCGAGTATATCATATGATGAGCAATAAATACTAC 180
QY 61 LeuAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
DB 181 GCAAGACTCCGCGAGAGCCGATTCACCATCTCCAGAGACATTCAGAGACACCTGTAT 240
QY 81 LeuGlnMetSerSerLeuLysSerGlyAspThrAlaLeuPheTyrCysAlaArgHisArg 100
DB 241 CTGCAATGACAGCCGAGAGCTGAGAGACAGAGCGGTGTATTAAGTGTGAGAGATCGG 300
QY 101 SerGlyTyr-----PheSerMetAspTyrTyrGlyGlnGlyThrSerValThr 116
DB 301 CACTCTACGATTTTGGAGTGGGTCTTCACTACTAGGGCCAGGGAACCTGTGACCC 360
QY 117 ValSerSer 119
DB 361 GTCTCTCTCA 369
```

Search completed: June 3, 2006, 09:17:13  
Job time: 16.5796 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 03:53:44 ; Search time 6305.61 Seconds  
(without alignments)  
3255.375 Million cell updates/sec

Title: US-10-635-908-15  
Perfect score: 1116  
Sequence: 1 DIVMTQSGRFMTTGVDRVS.....EVTHTGLSSPVTKSFNRGEC 214

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6366136 segs, 31973710525 residues  
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-Q=/abs/ABSSWEB.spool/US10635908/runat\_02062006\_104214\_10235/app\_query.fasta\_1  
-DB=GenEmbl -QFMT=faetap -SUFFIX=rge -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0  
-UNITS-bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h  
-USER=US10635908.@CCN\_1\_1\_5767\_@runat\_02062006\_104214\_10235 -NCPU=6 -ICPU=3  
-NO MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vl:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_da:\*  
  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1030	92.3	717 2	AX556961 Sequence
2	1030	92.3	717 2	AX709560 Sequence
3	1017	91.1	714 2	AR116649 Sequence

4	1017	91.1	714 2	BD069191
5	1017	91.1	714 2	CQ802834
6	1017	91.1	714 2	AR233008
7	1017	91.1	714 2	AR237939
8	1017	91.1	714 2	169460
9	1017	91.1	714 2	173079
10	1017	91.1	714 2	179264
11	1017	91.1	714 2	187038
12	1017	91.1	714 2	AR647560
13	1007	90.2	1501 2	CS239095
14	977.5	87.6	699 2	CS133169
15	962	86.2	4604 8	AJ852004
16	956	85.7	702 2	AX829027
17	954.5	85.5	711 2	DD163548
18	951	85.2	642 5	AB004304
19	948	84.9	642 2	AX329190
20	948	84.9	807 5	AB064078
21	945	84.7	748 2	AR566365
22	945	84.7	12190 2	CS101405
23	944	84.6	642 2	CS027619
24	943	84.5	660 2	AR139116
25	943	84.5	660 2	AR237916
26	942	84.4	793 5	AB064140
27	942	84.4	812 5	AB064043
28	942	84.4	812 5	AB064045
29	939.5	84.2	928 2	AX251598
30	939	84.1	2073 2	CQ904166
31	939	84.1	2082 2	CQ904163
32	937	84.0	759 5	AB064052
33	937	84.0	813 5	AB064081
34	936	83.9	642 5	AB027444
35	936	83.9	974 2	BD131246
36	936	83.9	974 2	AR589372
37	936	83.9	974 2	AX305000
38	936	83.9	974 2	AX306529
39	935	83.8	2193 2	CQ904169
40	935	83.8	2196 2	CQ904172
41	935	83.8	2166 2	CQ904175
42	935	83.8	5387 2	CQ904180
43	935	83.8	6620 2	CQ904178
44	935	83.8	7060 2	CQ904157
45	935	83.8	7171 2	CQ904160

## ALIGNMENTS

RESULT 1	AX556961	717 bp	DNA	linear	PAT 27-NOV-2002
LOCUS	AX556961	Sequence 16 from Patent WO02060955.			
DEFINITION	AX556961				
ACCESSION	AX556961				
VERSION	AX556961.1	GI:25900019			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE	1				
AUTHORS	Braslavsky,G.R., Hanna,N. and Chinn,P.				
TITLE	Modified antibodies and methods of use				
JOURNAL	Patent: WO 02060955-A 16 08-AUG-2002;				
FEATURES	Idac Pharmaceuticals Corporation (US)				
source	Location/Qualifiers				
	1..717				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Humanized C5E10 Light Chain Sequence"				

## ORIGIN

Alignment Scores: 6.08e-115 Length: 717  
Pred. No.: 1030.00 Matches: 198  
Score: 96.7% Conservative: 9  
Percent Similarity:

Best Local Similarity: 92.5% Mismatches: 7  
 Query Match: 92.3% Indels: 0  
 DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x AX556961 (1-717)

QY 1 AaplleValMetThrcInserGlnArgPheMetSerThrThrValGlyAspArgValSer 20  
 DB 73 GACATTGTGATATATCCAGTCTCAAAATTCATGTCCACATGATAGAGAGGGGTCAAC 132  
 QY 21 IletHrCysLysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40  
 DB 133 ATCACTCGAAGGCCAGTCAAGATGTGGTGGTCTGTGCTGCTGATCAACGAAACCA 192  
 QY 41 GlyInSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
 DB 193 GGACATCTCTCAACTACTGATTTACTGGTCACTCACCCGGACACTGGAGTCCCTGAT 252  
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80  
 DB 253 CGCTTCACAGGCGAGTGGATCTGGACAGATTCTCACTCAACATAGCAATGTGCACTCT 312  
 QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100  
 DB 313 GAAGACTTGGCAGATTAATTTCTGTCACTTATATAGCACTATCTCTCACGTTCCGAGGG 372  
 QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120  
 DB 373 GGAGCCAGAGTGAATTCAAAGTACGGTGGTGGACCACTGTCTTCACTTCCCGGCA 432  
 QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140  
 DB 433 TCTGATGAGCAGTGTGAATCTGGAAGTCTGTGTTGTGCTGTGTAATTAATCTTCTAT 492  
 QY 141 ProArgGlnAlaLysValGlnTyrLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
 DB 493 CCAGAGAGGCCAAAGTACAGTGAAGTGGATTAACCCCTCCAAATCCGGTATCTCCAG 552  
 QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
 DB 553 GAGAGTGTCAAGAGCAGCAGCAACAGACAGCAGCCTCAGCAGCAGCAGCAGCAGCAG 612  
 QY 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGly 200  
 DB 613 CTGAGCAAAAGCAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCAACCATCAGGGC 672  
 QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214  
 DB 673 CTGAGCTCGCCCTTCACAAAGACTTCAACAGGGAGAGTGT 714

RESULT 2  
 AX709560 717 bp DNA linear PAT 04-APR-2003  
 LOCUS Sequence 16 from Patent WO02096948.  
 DEFINITION AX709560  
 ACCESSION AX709560  
 VERSION AX709560.1 GI:29564980  
 KEYWORDS  
 ORGANISM  
 SOURCE  
 synthetic construct  
 synthetic construct  
 other sequences; artificial sequences.

REFERENCE  
 1 Braajawaky,G.R., Hanna,N., Chinn,P. and Hartharan,K.  
 AUTHORS Engineered tetravalent antibodies and methods of use  
 TITLE Patent: WO 02096948-A 16 05-DEC-2002;  
 JOURNAL Idex Pharmaceuticals Corporation (US)  
 location/Qualifiers

FEATURES  
 source 1..717  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Synthetic nucleotide sequence of CSE10 light chain"

ORIGIN

Alignment Scores:  
 Pred. No.: 6,08e-115 Length: 717  
 Score: 1030.00 Matches: 198  
 Percent Similarity: 96.7% Conservative: 9  
 Best Local Similarity: 92.5% Mismatches: 7  
 Query Match: 92.3% Indels: 0  
 DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x AX709560 (1-717)

QY 1 AaplleValMetThrcInserGlnArgPheMetSerThrThrValGlyAspArgValSer 20  
 DB 73 GACATTGTGATATATCCAGTCTCAAAATTCATGTCCACATGATAGAGAGGGGTCAAC 132  
 QY 21 IletHrCysLysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40  
 DB 133 ATCACTCGAAGGCCAGTCAAGATGTGGTGGTCTGTGCTGCTGATCAACGAAACCA 192  
 QY 41 GlyInSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
 DB 193 GGACATCTCTCAACTACTGATTTACTGGTCACTCACCCGGACACTGGAGTCCCTGAT 252  
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80  
 DB 253 CGCTTCACAGGCGAGTGGATCTGGACAGATTCTCACTCAACATTAAGCAATGTGCACTCT 312  
 QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100  
 DB 313 GAAGACTTGGCAGATTAATTTCTGTCACTTATATAGCACTATCTCTCACGTTCCGAGGG 372  
 QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120  
 DB 373 GGAGCCAGAGTGAATTCAAAGTACGGTGGTGGACCACTGTCTTCACTTCCCGGCA 432  
 QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140  
 DB 433 TCTGATGAGCAGTGTGAATCTGGAAGTCTGTGTTGTGCTGTGTAATTAATCTTCTAT 492  
 QY 141 ProArgGlnAlaLysValGlnTyrLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
 DB 493 CCAGAGAGGCCAAAGTACAGTGAAGTGGATTAACCCCTCCAAATCCGGTATCTCCAG 552  
 QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
 DB 553 GAGAGTGTCAAGAGCAGCAGCAACAGACAGCAGCCTCAGCAGCAGCAGCAGCAGCAG 612  
 QY 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGly 200  
 DB 613 CTGAGCAAAAGCAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCAACCATCAGGGC 672  
 QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214  
 DB 673 CTGAGCTCGCCCTTCACAAAGACTTCAACAGGGAGAGTGT 714

RESULT 3  
 AR116649 714 bp DNA linear PAT 16-MAY-2001  
 LOCUS Sequence 24 from patent US 6133426.  
 DEFINITION AR116649  
 ACCESSION AR116649  
 VERSION AR116649.1 GI:14096971  
 KEYWORDS  
 SOURCE  
 Unknown.  
 ORGANISM  
 Unclassified.

REFERENCE  
 1 (bases 1 to 714)  
 AUTHORS Gonzalez,T.N., Leong,S.R. and Presta,L.G.  
 TITLE Humanized anti-IL-8 monoclonal antibodies  
 JOURNAL Patent: US 6133426-A 24 17-OCT-2000;  
 location/Qualifiers

FEATURES  
 source 1..714  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN



## Alignment Scores:

Pred. No.: 2,29e-113 Length: 714  
 Score: 1017.00 Matches: 194  
 Percent Similarity: 96.3% Conservative: 12  
 Best Local Similarity: 90.7% Mismatches: 8  
 Query Match: 91.1% Indels: 0  
 DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x AB116649 (1-714)

```

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGCTCTCAAAATTCATGTCACATCAGTAGAGACGGGTACAC 129
QY 21 IletHrCyAlaAlaSerGlnAsnValValSerAlaValAlaTPrTyGlnGlnLysPro 40
DB 130 GTCACCTGCAGAGCCAGTCAAGATGGGTACTAATGTAGCCTGTATCAACAGAAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTCAAGACATGATTTACTGTCTATCTTACCGGTACAGTGAAGTCCCTGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGGACGATGATCTGGGACAGATTTCATCTCACCATCAGCATGTGACAGTCT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTPrThrPheGlyGly 100
DB 310 GAAGACTTGACAGACTATTTCTGTCTGCAATATACATCTATCTCTCTCAGTTCGCTCT 369
QY 101 GlyThrValLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 370 GGGACCAAGCTTGAGCTTGAGAGAGCTGTGGCTGCACATCTCTTCACTTCCGCCCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 430 TCTGATGACAGATGTAAATCTGGAACTGCTTCTGTGTGTGCTGCTGCAATATCTCTAT 489
QY 141 ProArgGlnAlaLysValGlnTPrLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCCAGAGAGGCCAAAGTATACGTGAAGGTGATACGCCCTCAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGAGGTGTCAAGAGCAGACAGACAGACAGACACCTACAGCTTCAGCAGACCTCGAGC 609
QY 181 LeuSerLysAlaAspTyrGlnLysShiLysValTyrAlaCysGlnValThrIleGlnGly 200
DB 610 CTGAGCAAGCAGACGATCTAGGAAACACAAAGTCTACGCTGCGAAGTCAACCCATCAGGGC 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyLys 214
DB 670 CTGAGCTCGCCCTGTCAACAAAGACCTTCACAGGAGGAGAGTGT 711

```

RESULT 4  
 BD069191 714 bp DNA linear PAT 27-AUG-2002  
 LOCUS BD069191  
 DEFINITION Antibody fragment-polymer conjugates and humanized anti-IL-8  
 monoclonal antibodies.  
 ACCESSION BD069191.1 GI:22614794  
 VERSION JP 2001512489-A/25.  
 KEYWORDS unidentifed  
 SOURCE unidentifed  
 ORGANISM unclassified sequences.  
 1 (bases 1 to 714)  
 Hsei,V., Kouments,I., Leong,S.R., Presta,L.G., Shahrokh,Z. and  
 Zapata,G.A.  
 TITLE Antibody fragment-polymer conjugates and humanized anti-IL-8  
 monoclonal antibodies  
 AUTHORS Patent: JP 2001512489-A 25 21-AUG-2001;  
 JOURNAL GENENTECH INC

## COMMENT

OS Unidentified  
 PN JP 2001512489-A/25  
 PD 21-AUG-2001  
 PF 20-FEB-1998 JP 1998536905  
 PR 21-FEB-1997 US 08/804444, 22-JAN-1998 US 09/012116 PI  
 VANESSA HSEI, IPIHGENIA KOUMENTS, STEVEN R LEONG, LEONARD G PI  
 PRESTA,  
 PI ZAHRA SHAHROKH, GERARDO A ZAPATA  
 PC C12N15/13, C07K19/00, A61K47/48, C07K16/24, C12N15/85, C12N5/10 CC  
 Strandedness: Double;  
 CC Topology: Linear;  
 CC Antibody fragment-polymer conjugates and humanized anti-IL-8  
 CC key monoclonal  
 CC antibodies  
 FT key location/Qualifiers  
 FT source 1..714 /organism='Unidentified'.  
 FT location/Qualifiers  
 1..714 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

## ORIGIN

```

Alignment Scores:
Pred. No.: 2,29e-113 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x BD069191 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGCTCTCAAAATTCATGTCACATCAGTAGAGACGGGTACAC 129
QY 21 IletHrCyAlaAlaSerGlnAsnValValSerAlaValAlaTPrTyGlnGlnLysPro 40
DB 130 GTCACCTGCAGAGCCAGTCAAGATGGGTACTAATGTAGCCTGTATCAACAGAAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTCAAGACATGATTTACTGTCTATCTTACCGGTACAGTGAAGTCCCTGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGGACGATGATCTGGGACAGATTTCATCTCACCATCAGCATGTGACAGTCT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTPrThrPheGlyGly 100
DB 310 GAAGACTTGACAGACTATTTCTGTCTGCAATATACATCTATCTCTCTCAGTTCGCTCT 369
QY 101 GlyThrValLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 370 GGGACCAAGCTTGAGCTTGAGAGAGCTGTGGCTGCACCATCTGTCTTCACTTCCGCCCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 430 TCTGATGACAGATGTAAATCTGGAACTGCTTCTGTGTGTGCTGCTGCAATATCTCTAT 489
QY 141 ProArgGlnAlaLysValGlnTPrLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCCAGAGAGGCCAAAGTATACGTGAAGGTGATACGCCCTCAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGAGGTGTCAAGAGCAGACAGACAGACAGACACCTACAGCTTCAGCAGACCTCGAGC 609
QY 181 LeuSerLysAlaAspTyrGlnLysShiLysValTyrAlaCysGlnValThrIleGlnGly 200
DB 610 CTGAGCAAGCAGACGATCTAGGAAACACAAAGTCTACGCTGCGAAGTCAACCCATCAGGGC 669

```

QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214  
Db 670 CTGAGCTGCCCGTCCAAAGAGCTTCAACAGGGAGAGGTGT 711

RESULT 5  
LOCUS CQ802834 714 bp DNA linear PAT 10-MAY-2004  
DEFINITION Sequence 24 from Patent EP1415998.  
ACCESSION CQ802834  
VERSION CQ802834.1 GI:47109852  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
AUTHORS Heel,V., Koumenis,I., Leong,S.R., Presta,L.R., Shahrokh,Z. and Zapata,G.A.  
TITLE Antibody fragment-polymer conjugates and humanized anti-IL-8  
JOURNAL monoclonal antibodies  
Genetech, Inc. (US)  
Genetech, Inc. (US)  
FEATURES  
source 1..714  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Alignment Scores:  
Pred. No.: 2,296-113 Length: 714  
Score: 1017.00 Matches: 194  
Percent Similarity: 96.3% Conservative: 12  
Best Local Similarity: 90.7% Mismatches: 8  
Query Match: 91.1% Indels: 0  
DB: 2 Gaps: 0  
US-10-635-908-15 (1-214) x CQ802834 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20  
Db 70 GATATCGTCATGACACAGCTCCAAATAATTCATGTCACATCAGTAGAGACAGGCTCAGC 129

QY 21 IleThrCysLysAlaSerGlnAsnValAlaSerAlaValAlaTrpTyrGlnIleuPro 40  
Db 130 GTACCTCGAAGGCCAGATGAGATGGGTACTAATGTAAGCTGGATCAACAGAAACCA 189

QY 41 GlyIleuSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
Db 190 GGGCAATCTCCCTAAAGCACTGATTTACTGTCATCTCCGCTACAGTGGAGTCCCTGAT 249

QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80  
Db 250 CCCTTCACAGGAGGAGTCTGGGACAGATTTCATCTCACCATCAGCATGTGCACTGT 309

QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100  
Db 310 GAAGACTTGGCAGACTATTCTGTGTCAGCAATATATATCTCTCTCCGTTCCGTTCT 369

QY 101 GlyThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120  
Db 370 GGGACCAAGCTCGAGCTTGAAGAGCTGGCTGCACCATCTGTCTTCTTCCCGCA 429

QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValAlaCysLeuLeuAsnAsnPheTyr 140  
Db 430 TCTGATGACACTTGAATCTGGAATCTGCTTGTGTGCTGCTGCTGAATTAATCTTCT 489

QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyValAsnSerGln 160  
Db 490 CCACAGAGAGCCAAAGTACAGTGAAGGTGAGTAACGCCCTCCAAATCGGGTAATCTCCAG 549

QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180

Db 550 GAGAGTGTACAGACGACGACAGCAAGGACAGCACTACAGCTTCAGACACCTCTGACG 609

QY 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGluValThrHisGlnIle 200  
Db 610 CTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCTCGAAGTCAACCATCAGGAC 669

QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214  
Db 670 CTGAGCTGCCCGTCCAAAGAGCTTCAACAGGGAGAGGTGT 711

RESULT 6  
LOCUS AR233008 714 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 24 from patent US 6458355.  
ACCESSION AR233008  
VERSION AR233008.1 GI:27275392  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS Heel,V., Koumenis,I., Leong,S., Presta,L., Shahrokh,Z. and Zapata,G.  
TITLE Methode of treating inflammatory disease with anti-IL-8 antibody  
JOURNAL fragment-polymer conjugates  
Genetech, Inc.; South San Francisco, CA  
Genetech, Inc. (US)  
FEATURES  
source 1..714  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 2,296-113 Length: 714  
Score: 1017.00 Matches: 194  
Percent Similarity: 96.3% Conservative: 12  
Best Local Similarity: 90.7% Mismatches: 8  
Query Match: 91.1% Indels: 0  
DB: 2 Gaps: 0  
US-10-635-908-15 (1-214) x AR233008 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20  
Db 70 GATATCGTCATGACACAGCTCCAAATAATTCATGTCACATCAGTAGAGACAGGCTCAGC 129

QY 21 IleThrCysLysAlaSerGlnAsnValAlaSerAlaValAlaTrpTyrGlnIleuPro 40  
Db 130 GTACCTCGAAGGCCAGATGAGATGGGTACTAATGTAAGCTGGATCAACAGAAACCA 189

QY 41 GlyIleuSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
Db 190 GGGCAATCTCCCTAAAGCACTGATTTACTGTCATCTCCGCTACAGTGGAGTCCCTGAT 249

QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80  
Db 250 CCCTTCACAGGAGGAGTCTGGGACAGATTTCATCTCACCATCAGCATGTGCACTGT 309

QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100  
Db 310 GAAGACTTGGCAGACTATTCTGTGTCAGCAATATATATCTCTCTCCGTTCCGTTCT 369

QY 101 GlyThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120  
Db 370 GGGACCAAGCTCGAGCTTGAAGAGCTGGCTGCACCATCTGTCTTCTTCCCGCA 429

QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValAlaCysLeuLeuAsnAsnPheTyr 140  
Db 430 TCTGATGACACTTGAATCTGGAATCTGCTTGTGTGCTGCTGCTGAATTAATCTTCT 489

QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyValAsnSerGln 160

DB 490 CCCAGAGAGCCAAAGTACAGTGAAGTGGATTAACCCCTCCATCGGGTAACTCCAG 549

QY 161 GUSerValThrgluGlnAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 180

DB 550 GAGAGTGTACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 609

QY 181 LeuSerLysAlaAspTyGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200

DB 610 CTGAGCAAGCAGACACTACGAGAAACAAAGTCTACGCTGCGAGTCAACCCATCAGAGGC 669

QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214

DB 670 CTGAGCTCGCCCGTCAACAAAGAGCTTCAACAGGGAGAGTGT 711

RESULT 7

AR237939 714 bp DNA linear PAT 20-DEC-2002

LOCUS AR237939

DEFINITION Sequence 24 from patent US 6468532.

ACCESSION AR237939

VERSION AR237939.1 GI:27282809

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 714)

AUTHORS Hseil,V., Koumenis,I., Leong,S., Presta,L., Shahrokhi,Z. and Zapata,G.

TITLE Methods of treating inflammatory diseases with anti-IL-8 antibody

JOURNAL Fragment-polymer conjugates

Genentech, Inc.; South San Francisco, CA

Patent: US 6468532-A 24 22-OCT-2002;

Location/Qualifiers

1. 714

FEATURES

source /organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 2.29e-113 Length: 714

Score: 1017.00 Matches: 194

Percent Similarity: 96.3% Conservative: 12

Best Local Similarity: 90.7% Mismatches: 8

Query Match: 91.1% Indels: 0

DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x AR237939 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrValGlyAspArgValSer 20

DB 70 GATATCGTCATGACACAGTCTCAAAATTCATGTCACATCAGTAGAGACAGGGTCAGC 129

QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTPrpYrGlnGlnLysPro 40

DB 130 GTCACTGCAAGGCGACGATCGAATGCGTATCTAATGTAGCTGTATCAACAGAAACCA 189

QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60

DB 190 GGGCAATCTCTTAAGACGATGATTTACTGTCATCTTACCGGTACAGGAGTCCCTGAT 249

QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80

DB 250 CGCTTCAACAGGACGATGATCTGGAGAGATTTCATCTCACATCAGCATGTCAGTCT 309

QY 81 GlnAspLeuAlaAspPhePheCysGlnGlnIleTyrSerAsnTyrProTPrpThrPheGlyGly 100

DB 310 GAAGACTTGGCAGACTATTTCTGTCAGCAATATATACATCTATCTTCCACGTTGGTCT 369

QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120

DB 370 GGGCAAGCTGAGGACTTCGAAAGAGCTGTGCTGCACCATCTGCTTCATCTTCCCGCA 429

QY 121 SerAspGlnIleLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140

DB 430 TCTGATGACAGATTGAAATCTGGAATCTGCTTGTGTGTGCTGTAATACTTCTAT 489

QY 141 ProArgGluAlaLysValGlnTPrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160

DB 490 CCCAGAGAGCCAAAGTACAGTGAAGTGGATTAACCCCTCCATCGGGTAACTCCAG 549

QY 161 GUSerValThrgluGlnAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 180

DB 550 GAGAGTGTACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 609

QY 181 LeuSerLysAlaAspTyGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200

DB 610 CTGAGCAAGCAGACACTACGAGAAACAAAGTCTACGCTGCGAGTCAACCCATCAGAGGC 669

QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214

DB 670 CTGAGCTCGCCCGTCAACAAAGAGCTTCAACAGGGAGAGTGT 711

RESULT 8

169460 714 bp DNA linear PAT 04-FEB-1998

LOCUS 169460

DEFINITION Sequence 27 from patent US 5677426.

ACCESSION 169460

VERSION 169460.1 GI:2831582

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 714)

AUTHORS Fong,S., Hebert,C., Alice., Kim,K., Jin. and Leong,S.R.

TITLE Anti-IL-8 antibody fragments

JOURNAL Patent: US 5677426-A 27 14-OCT-1997;

Location/Qualifiers

1. 714

FEATURES

source /organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 2.29e-113 Length: 714

Score: 1017.00 Matches: 194

Percent Similarity: 96.3% Conservative: 12

Best Local Similarity: 90.7% Mismatches: 8

Query Match: 91.1% Indels: 0

DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x 169460 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrValGlyAspArgValSer 20

DB 70 GATATCGTCATGACACAGTCTCAAAATTCATGTCACATCAGTAGAGACAGGGTCAGC 129

QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTPrpYrGlnGlnLysPro 40

DB 130 GTCACTGCAAGGCGACGATCGAATGCGTATCTAATGTAGCTGTATCAACAGAAACCA 189

QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60

DB 190 GGGCAATCTCTTAAGACGATGATTTACTGTCATCTTACCGGTACAGGAGTCCCTGAT 249

QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80

DB 250 CGCTTCAACAGGACGATGATCTGGAGAGATTTCATCTCACATCAGCATGTCAGTCT 309

QY 81 GlnAspLeuAlaAspPhePheCysGlnGlnIleTyrSerAsnTyrProTPrpThrPheGlyGly 100

DB 310 GAAGACTTGGCAGACTATTTCTGTCAGCAATATATACATCTATCTTCCACGTTGGTCT 369

QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120

DB 370 GGGCAAGCTGAGGACTTCGAAAGAGCTGTGCTGCACCATCTGCTTCATCTTCCCGCA 429

QY 121 SerAspGlnIleLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140

```
Db      430  TCTGATGACGACGTGAAATCTGAACTGCTTCTGTGTGCTGCTGTAATTAATTCTAT 489
Qy      141  ProA:GGLUALAlaValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db      490  CCCAGAGAGGCCAAAGTACAGTGAAGGTGATTAACGCCCTCCAAATCGGGTAATCTCCAG 549
Qy      161  GluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db      550  GAGAGTGTCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 609
Qy      181  LeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200
Db      610  CTGAGCAAGACAGACTACGAGAAACACAAAGCTTACGCTTGCAGAACTCACCATCGAGGC 669
Qy      201  LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
Db      670  CTGAGCTGCCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGT 711
```

## RESULT 9

```
LOCUS      I73079          714 bp      DNA      linear      PAT 03-APR-1998
DEFINITION Sequence 27 from patent US 5686070.
ACCESSION  I73079
VERSION     I73079.1  GI:3009218
KEYWORDS
```

SOURCE  
ORGANISM

Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 714)  
Doetschuk, C.M., Fong, S., Hebert, C., Alice, Kim, K., Jin, and Leong, S.R.

AUTHORS  
TITLE  
METHODS  
PATENT: US 5686070-A 27 11-NOV-1997;

JOURNAL  
FEATURES  
LOCATION/Qualifiers  
1. 714

source  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 2,29e-113 Length: 714  
Score: 1017.00 Matches: 194  
Percent Similarity: 96.3% Conservative: 12  
Best Local Similarity: 90.7% Mismatches: 8  
Query Match: 91.1% Indels: 0  
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x I73079 (1-714)

```
Qy      1  AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db      70  GATATGTCATGACACAGTCTCAAAAATTCATGTCACATCAGTAGAGACAGGGTCAAG 129
Qy      21  IleThrCysLysValSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
Db      130  GTCACTTCGAAAGCCAGTCAAGATGTGGTACTTAAGTAACTGCTGATCAACGAAACCA 189
Qy      41  GlyGlnSerProLysLeuLeuLysTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db      190  GGGCAATCTCTTAAGACATGATTTACTGTCATCTACCGGTACAGTGAAGTCCCTGAT 249
Qy      61  ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db      250  CGCTTCACAGGCGAGTGAATCTGGACAGATTTCATCTCACATCGCCATGTGCAAGTCT 309
Qy      81  GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
Db      310  GAAGACTTGGCAACATATTTCTGTCAACATATTAACATCTATCTCTCACGTTCCGTCCT 369
Qy      101  GlyThrLysLeuGlnLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db      370  GGGACCAAGCTGGAGCTTGAAGAGCTGTGGCTGCACCATCTGTCTTCACTTCCCGCCA 429
```

```
Qy      121  SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
Db      430  TCTGATGACGACGTGAAATCTGAACTGCTTCTGTGTGCTGCTGTAATTAATTCTAT 489
Qy      141  ProA:GGLUALAlaValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db      490  CCCAGAGAGGCCAAAGTACAGTGAAGGTGATTAACGCCCTCCAAATCGGGTAATCTCCAG 549
Qy      161  GluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db      550  GAGAGTGTCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 609
Qy      181  LeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200
Db      610  CTGAGCAAGACAGACTACGAGAAACACAAAGCTTACGCTTGCAGAACTCACCATCGAGGC 669
Qy      201  LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
Db      670  CTGAGCTGCCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGT 711
```

## RESULT 10

```
LOCUS      I79264          714 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 27 from patent US 5707622.
ACCESSION  I79264
VERSION     I79264.1  GI:3207554
KEYWORDS
```

SOURCE  
ORGANISM

Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 714)  
Fong, S., Hebert, C., Alice, Kim, K., Jin, and Leong, S.R.

AUTHORS  
TITLE  
METHODS  
PATENT: US 5707622-A 27 13-JAN-1998;

JOURNAL  
FEATURES  
LOCATION/Qualifiers  
1. 714

source  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 2,29e-113 Length: 714  
Score: 1017.00 Matches: 194  
Percent Similarity: 96.3% Conservative: 12  
Best Local Similarity: 90.7% Mismatches: 8  
Query Match: 91.1% Indels: 0  
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x I79264 (1-714)

```
Qy      1  AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db      70  GATATGTCATGACACAGTCTCAAAAATTCATGTCACATCAGTAGAGACAGGGTCAAG 129
Qy      21  IleThrCysLysValSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
Db      130  GTCACTTCGAAAGCCAGTCAAGATGTGGTACTTAAGTAACTGCTGATCAACGAAACCA 189
Qy      41  GlyGlnSerProLysLeuLeuLysTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db      190  GGGCAATCTCTTAAGACATGATTTACTGTCATCTACCGGTACAGTGAAGTCCCTGAT 249
Qy      61  ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db      250  CGCTTCACAGGCGAGTGAATCTGGACAGATTTCATCTCACATCGCCATGTGCAAGTCT 309
Qy      81  GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
Db      310  GAAGACTTGGCAACATATTTCTGTCAACATATTAACATCTATCTCTCACGTTCCGTCCT 369
Qy      101  GlyThrLysLeuGlnLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db      370  GGGACCAAGCTGGAGCTTGAAGAGCTGTGGCTGCACCATCTGTCTTCACTTCCCGCCA 429
```

```

QY 121 SerAspGluGlnLeuIysSerGlyThrAlaSerValCysLeuLeuAsnAspPheTyr 140
DB 430 TCGATGACAGAGTTGAATCTGAAGCTGCTGTGTGTGCTGCTGTAATTAATTCTTAT 489
QY 141 ProArgGluAlaIleValGlnTyrPheValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCAGAGAGGCCAAAGTACAGTGGAGGTGGATTAAGCCCTCCCAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGlnIleAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGAGTGTCAACAGAGCAGACAGACAGACAGCCTTACAGCCTTACAGCAGCCTTACAG 609
QY 181 LeuSerLysAlaAspTyrGluLysHisIleValTyrAlaCysGluValThrHisGlnGly 200
DB 610 CTAGCAAGACAGACTACGAGAAACACAAAGTCTTACCTTCCAGAGTCACTCCATCAGGC 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
DB 670 CTGAGCTCGCCCTGCAAAAGAGCTTCAACAGGGGAGAGTGT 711

RESULT 11
187038 714 bp DNA linear PAT 10-JUN-1998
LOCUS Sequence 27 from patent US 5702946.
DEFINITION 187038
ACCESSION 187038.1 GI:3206756
VERSION 187038.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 714)
AUTHORS Doerschuk, C.M., Fong, S., Hebert, C.Alice, Kim, K.Jin, and Leong, S.R.
TITLE Anti-IL-8 monoclonal antibodies for treatment of inflammatory disorders
JOURNAL Patent: US 5702946-A 27 30-DEC-1997;
FEATURES
source location/Qualifiers
1..714
/mol_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2.29e-113 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 0
DB: 2

US-10-635-908-15 (1-214) x 187038 (1-714)
QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGCTCTCAAAATTCATGTCACATCATGAGAGACAGGGTCCAGC 129
QY 21 IleThrCysIleValAspSerGlnAsnValAlaSerAlaValAlaTyrGlnGlnLysPro 40
DB 130 GTCACTGTCAAGGCCAGTCAGAAATGTGGTACTAAATGATGAGCTGTATCAACAGAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTTAAGCACTGATTTACTGTCATCTTACCGGTACAGGAGTCCCTGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGCAGGAGTGTGGAGCAGATTTCACTTCCATCAGCCATGAGCATGTGCAAGTCT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrThrPheGlyGly 100
DB 310 GAAGCTTGACAGACTATTTCTGTCAACAATTAATCACTATCTCTCCACGTTCCGTTCT 369
QY 101 GlyThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePhePro 120

```

```

DB 370 GGGACCAAGCTGAGCTTGAAGAGCTGTGGCTGACCACTGTCTTCACTTCCGCCCA 429
QY 121 SerAspGluGlnLeuIysSerGlyThrAlaSerValCysLeuLeuAsnAspPheTyr 140
DB 430 TCGATGACAGAGTTGAATCTGAAGCTGCTGTGTGTGCTGCTGTAATTAATTCTTAT 489
QY 141 ProArgGluAlaIleValGlnTyrPheValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCAGAGAGGCCAAAGTACAGTGGAGGTGGATTAAGCCCTCCCAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGlnIleAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGAGTGTCAACAGAGCAGACAGACAGACAGCCTTACAGCCTTACAGCAGCCTTACAG 609
QY 181 LeuSerLysAlaAspTyrGluLysHisIleValTyrAlaCysGluValThrHisGlnGly 200
DB 610 CTAGCAAGACAGACTACGAGAAACACAAAGTCTTACCTTCCAGAGTCACTCCATCAGGC 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
DB 670 CTGAGCTCGCCCTGCAAAAGAGCTTCAACAGGGGAGAGTGT 711

RESULT 12
AR647560 714 bp DNA linear PAT 20-APR-2005
LOCUS AR647560
DEFINITION AR647560
ACCESSION AR647560
VERSION AR647560.1 GI:62786643
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 714)
AUTHORS Heel, V., Koumentis, I., Leong, S.R., Presta, L.G., Shahrokh, Z. and Zapata, G.A.
TITLE Antibody fragment-polymer conjugates and humanized anti-IL-8 monoclonal antibodies
JOURNAL Patent: US 6870033-A 24 22-MAR-2005;
FEATURES
source location/Qualifiers
1..714
/mol_type="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2.29e-113 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 0
DB: 2

US-10-635-908-15 (1-214) x AR647560 (1-714)
QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGCTCTCAAAATTCATGTCACATCATGAGAGACAGGGTCCAGC 129
QY 21 IleThrCysIleValAspSerGlnAsnValAlaSerAlaValAlaTyrGlnGlnLysPro 40
DB 130 GTCACTGTCAAGGCCAGTCAGAAATGTGGTACTAAATGATGAGCTGTATCAACAGAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTTAAGCACTGATTTACTGTCATCTTACCGGTACAGGAGTCCCTGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGCAGGAGTGTGGAGCAGATTTCACTTCCATCAGCCATGAGCATGTGCAAGTCT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrThrPheGlyGly 100

```

Db	310	GAAAGCTTGGCAGACTATTTCCTGTGCAGCAATTATACATCTATCCCTCAAGTTGGTCT	369
Qy	101	GIYThrIyLLeuGIuIleIyAArgThrValAlaAlaProSerValPheIlePheProPro	120
Db	370	GGGACCAAGCTGGAGCTTCGAAAGAGCTGGCTGGTGCACATCTGCTTCATCTTCCCGCA	429
Qy	121	SerAAspGIuGIuLeuIySeSerGIYThrAlaSerValValCyLLeuLeuAAspMheTy	140
Db	430	TCTGATGAGCACTTGAATCTCGAAGCTGCTTGTGTGTGTCTCTGTAATTAATCTTCTAT	489
Qy	141	ProAArgIuAlaIyLValGIuIleTPrIyValAAspAAsnAlaLeuGIuIleSeGIyAAsnSerGI	160
Db	490	CCCAAGAGAGGCCAAAGTACAGTGAAGGTGATTAACGCCCTTCATCCGGTAACTCCAG	549
Qy	161	GIuSerValIThGIuGIuAAspSerIyAAspSerIThTySerLeuSerSerIThLeuThr	180
Db	550	GAGAGTGTACAGACAGACAGACAGACAGACACACACTTAAGCTTACAGACAGACCTTGACG	609
Qy	181	LeuSerIyAlaAAspTyTGIuIyShIyIyValITyAlaCyGSIuValIThThIleGIuIy	200
Db	610	CTGACCAAAAGCAGACTACAGAAAACAAAGTCTACGCTCGGAAGTCAACCATCAGAGC	669
Qy	201	LeuSerSerProValIThIySerPheAAsnAArgIyGIuCyS	214
Db	670	CTGAGCTCGCCGCTCAAAAGAGCTTCAACAGGGAGAGTGT	711
RESULT 13			
CS239095	1701 bp	DNA	linear
LOCUS	Sequence 10 from Patent WO2005108989.		PAT 04-JAN-2006
DEFINITION	CS239095		
ACCESSION	CS239095.1		
VERSION	GI:84365467		
KEYWORDS			
SOURCE			
ORGANISM	Mus musculus (house mouse)		
	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
	Sciurognathi; Murioidea; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Chuncharapai, A.		
JOURNAL	Patent: WO 2005108989-A 10 17-NOV-2005;		
FEATURES			
source	Location/Qualifiers		
	1..1701		
	/organism="Mus musculus"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:10090"		
	1684		
	unseq		
	/note="unknown amino acid"		
ORIGIN			
Alignment Scores:			
Pred. No.:	1,06e-111	Length:	1701
Score:	1007.00	Matches:	193
Percent Similarity:	95.3%	Conservative:	11
Best Local Similarity:	90.2%	Mismatches:	10
Query Match:	2	Indels:	0
DB:		Gaps:	0
US-10-635-908-15 (1-214) x CS239095 (1-1701)			
Qy	1	AspIleValMetThrGlnSerGlnAArgPheMetSerIThThrValGIyAAspArgValSer	20
Db	109	GATATCGTATGATGCCAGTCTCAAGATTCATGTCACATCCATGAGACAGGGTCAAC	168
Qy	21	IleThrCyAlaIyAlaSerGlnAAsnValValSerAlaValAlaITyITyGIuIleIyIy	40
Db	169	GTCACCTGCAGGCCAGCTCAGACTGTGATTAATGTAGCTCGATATCAACAGAAACTA	228
Qy	41	GIyGlnSerProIyLeuLeuIleITySerAlaSerAAsnArgITyThrGIyValProAAsp	60
Db	229	GGGCAATCTCTTAAACACACTGATTTAATCTGGGATCTCAACGGGTGATGGGGATCCCTGAT	288

Oy	61	ArgPheThrGlySerGlySerGlyYThrAspPheThrLeuThrIleSerAsnMetGlnSer	80
Db	289	CGCTTCACAGGACGTGGATCTCGGACGATTTTCACTTCCACCATCAGCAATGTGCACT	348
Oy	81	GluAspLeuAlaAspPhePheCysGlnGlnIleTyrSerAsnTyrProTPrThrPheGlyGly	100
Db	349	GAAGACTTGGCAGAGTATTTCTGTGCACCAATATTCACAGTTTCCGTGGACGTTCCGTGA	408
Oy	101	GlyThrIleLeuGlnIleLeuValGlyThrValAlaAlaProSerValPheIlePheProPro	120
Db	409	GGTACCAAGGTGGAGATCAACGAACTGTGGCTGGACCAATCTGTTCATCTTCCGCCCA	468
Oy	121	SerAspGlnGlnLeuIleuIleuSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr	140
Db	469	TCTGATAGACAGTTTGAATCTGGAACTGCTTCTGTTGTGGCCGTGCAATTACTTAT	528
Oy	141	ProArgGluAlaIleuValGlnTPrPLeuValAspAsnAlaLeuGlnSerGlyAsnSerGln	160
Db	529	CCCGAGAGAGGCCAAAGTACAGTGGAGAGTGAATACCCCTCCCAATGGGGTAATCCACG	588
Oy	161	GluSerValThrGlnGlnAspSerLeuAspSerThrTyrSerLeuSerSerThrLeuThr	180
Db	589	GAGGTGTTCACAGGACGACGACGAGAAAGACACGACCTTACAGCTCAGACGACCTTACG	648
Oy	181	LeuSerTyrAlaAspTyrGluTyrSHIleuValTyrAlaCysGluValIleThrIleGlnGly	200
Db	649	CTGAGCAAAAGACAGCTACGAGAAACACAAAGTCAACGCTCGGAGAGTCAACCATCAGGCG	708
Oy	201	LeuSerSerProValThrIleSerPheAsnArgIleGlyCys	214
Db	709	CTGAGCTTCGCCCGCTCACAAAGAGCTTCAACAGGGGAGAGTGT	750
RESULT 14			
LOCUS	CS133169	699 bp	DNA
DEFINITION	Sequence 14 from Patent WO2005063299.	linear	PAT 02-AUG-2005
ACCESSION	CS133169		
VERSION	CS133169.1	GI:71792256	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
JOURNAL	Hominidae; Homo.		
FEATURES	1 Chang, W.		
SOURCE	Compositions and methods for the treatment of tumor of hematopoietic origin Patent: WO 2005063299-A 14 14-JUL-2005; Genentech, Inc. (US)		
ORIGIN	Location/Qualifiers		
	1..699		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Alignment Scores:	1..4e-108	Length:	699
Pred. No.:	977..50	Matches:	190
Score:	98.4%	Conservative:	12
Percent Similarity:	98.4%	Mismatches:	11
Best Local Similarity:	87.6%	Indels:	1
Query Match:	2	Gaps:	1
DB:			
US-10-635-908-15 (1-214) x CS133169 (1-699)			
Oy	1	AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer	20
Db	58	GATATCGGATGACCCAGCTTCATTAATTTATGTCACATCAGTAGAGGACAGGGGTGACG	117
Oy	21	IleThrCysArgAlaSerGlnAsnValValSerAlaValAlaTPrTyrGlnGlnIlePro	40

```

Db      118 ATCTCCGCAAGCCAGTCAGATGAGTTCTGTGATCCCTGATCAACAGAGCCCA 177
Qy      41  GylGlnSerProTylsleuLeuLeuTyrSerAlaSerAspArgTyrThrGlyValProAsp 60
Db      178 GGACATCTCCCTAACTACTGATTTACTCG--GATACCGGATCACTAGATCCCTGAT 234
Qy      61  ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db      235 CGCTTCACTGGCAGTGGATCTGGAGACGATTTCACTTCACTCACTACAGACGTGCGAGCT 294
Qy      81  GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrThrPheGlyGly 100
Db      295 GAAGACCTGGCATTTATTTCTGTCAAGCAACATTATGACTCTCATTCACTCAGCTCGGCTCG 354
Qy      101 GlyThrIleLeuGlnIleTyrArgThrValAlaAlaProSerValPheIlePheProPro 120
Db      355 GGATCCAAAGGTGAGATCAACGAACTGTGCTGACCATCTGCTTCACTTCCCGCCA 414
Qy      121 SerAspGlnGlnLeuTylsSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
Db      415 TCTGATAGCAGATTGAATCTGGAACCTCTTCTGTGTGCTGCTGATTAATCTTCTAT 474
Qy      141 ProArgGlnAlaTyrValGlnTyrPlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db      475 CCCAGAGAGGCCAAAGATACAGTGAAGTGATTAACCCCTCCATCGGGTAACTCCACG 534
Qy      161 GluSerValThrGlnGlnAspSerTylsAspSerThrTyrTyrSerLeuSerSerThrLeuThr 180
Db      535 GAGAGTGTCAAGAGCAGACAGCAGACAGCACCCTACAGCTCAGACAGACCTTACG 594
Qy      181 LeuSerTyrAlaAspTyrGlnTylsIleTyrAlaTyrAlaCysGlnValThrIleGlnGly 200
Db      595 CTGAGCAAGCAGACTCGAGAAACAAAGATCACTCCCTCGGAAGTCAACCCATCAGAGCC 654
Qy      201 LeuSerSerProValThrTylsSerPheAsnArgGlyGlnCys 214
Db      655 CTGAGCTCGCCCTCAACAAAGAGCTTCAACAGCGGAGAGTGT 696

RESULT 15
AJ852004      4604 bp      DNA      circular SYN 08-JAN-2005
LOCUS      Synthetic construct pASK88-huHRS3-VH-EP3/1 for humanized anti-CD30
DEFINITION      Fab fragment.
ACCESSION      AJ852004.1 GI:57337318
VERSION      beta lactamase; bla gene; Fab fragment; heavy chain; IGHG1 gene;
KEYWORDS      IGH gene; light chain; tet repressor; tetr gene.
SOURCE      Cloning vector pASK88-huHRS3-VH-EP3/1
ORGANISM      other sequences; artificial sequences; vectors.
REFERENCE      1
AUTHORS      Schlapschky M.
TITLE      Immunization of an anti-CD30 Fab Fragment as a reagent for the
            immunotherapy of Hodgkin's Lymphoma
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 4604)
AUTHORS      Schlapschky M.
TITLE      Direct Submission
JOURNAL      Submitted (22-OCT-2004) Schlapschky M., LS Biologische Chemie, TU
            Muenchen, An der Saatzeit 5, 85354 Freising, GERMANY
FEATURES
            source
            1..4604
                /organism="Cloning vector pASK88-huHRS3-VH-EP3/1"
                /mol_type="Other DNA"
                /db_xref="taxon:299811"
                /rearranged
                /lab_host="Escherichia coli"
                /note="tet promoter region"
            45..50
            -35_signal
            -10_signal
            RBS
            95..97

```

```

RBS      136..139
gene      147..908
            /gene="IGHG1"
CDS      147..908
            /gene="IGHG1"
            /note="VH and CH1 domains
            mouse-human chimera
            His6 tag for IMAC purification"
            /codon_start=1
            /product="Fab fragment heavy chain precursor"
            /db_xref="GI:57337319"
            /protein_id="CAH65830.1"
            /translation="MKRTIALAVALAGRTVAQAEVRLQESGGGLVPGGSLRSA
            ASGFTFTYTHIHWKQAEKGLWSTINPSGISDYNQFRGRFTTSANKSKNTAYL
            QNNSLRABDTAVYYCARADYGNKYTWPPYGGTLTVSSASSTKSPVPLAPSSK
            STSGTALAGCLVKDYFPEPTVSNMGSALTGVHFPFPAVLQSSGLYSLSVTVPS
            SLGTQYICNVNHNKPSNTKVDKVEPKSGHHHHH"
            147..209
            /gene="IGHG1"
            /note="ompa signal peptide"
            210..905
            /gene="IGHG1"
            /product="Fab fragment heavy chain"
            916..919
            928..1635
            /gene="IGHK"
            928..1635
            /gene="IGHK"
            /note="mouse-human chimera"
            /codon_start=1
            /transl_table=11
            /product="light chain precursor"
            /protein_id="CAH65831.1"
            /db_xref="GI:57337320"
            /translation="MKOSTIALALPLFPYTKADIELTQSSPSLSASVDRTTIC
            KASQNVGNVAVYQQRGKAPKYLISASVRSVRSRSGSGSDFTLTSLQPE
            DEATVYCOQHHTPLTFGGGTKEIKRTAAAPSVFPPEDBDLKSQTASVCLLNPF
            YPERARVQMKVDNALQSGNSQESVTPDSKDSYSTLSLTLTKADIEKRYACEVT
            HQGLSPVTSFNNRGC"
            928..990
            /gene="IGHK"
            /note="phoa signal peptide"
            991..1632
            /gene="IGHK"
            /product="light chain"
            1647..1721
            /note="lipoprotein transcription terminator"
            1723..2168
            /note="intergenic region of filamentous phage f1"
            2310..3170
            /gene="bla"
            2310..3170
            /gene="bla"
            /codon_start=1
            /transl_table=11
            /product="beta lactamase"
            /protein_id="CAH65832.1"
            /db_xref="GI:57337321"
            /translation="MSIQHFRVALTLPFAFCLPVPAHPTLVKVKADPOLGARVGY
            IEDLNSGKILSEFRPEERPPMSTFRVILACGAVLSIDAGQELGRIRHYSQNDLVE
            YSPVTEKHLDGWTRELCSAITMSDNTANLLLTITGGKEILTALHNKGDIYTRL
            DRWPELNEBAIPNDERDTMPVAMATLRLLTGLLELTLASRQQLIDWEDADKVGAPL
            LRSLAPAGWFIADKSGAGERSGIIALGPDGKPSRIIVITYTGSQATDERNRQIA
            EIGSLIKHW"
            3180..3803
            /gene="tetr"
            3180..3803
            /gene="tetr"
            /codon_start=1
            /transl_table=11
            /product="tet repressor"
            /protein_id="CAH65833.1"

```





GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 03:51:33 ; Search time 698.553 Seconds  
(without alignments)  
3203.899 Million cell updates/sec

Title: US-10-635-908-15  
Perfect score: 1116  
Sequence: 1 DIVMTQSGQFMSTVTGDRVS.....EVTGQGLSSPTVKSFNRGEC 214

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues  
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frimex\_p2n.model -DEV=xlh  
-Q=/abs/ABSSWEB.spool/US10635908/runat\_02062006\_104212\_10223/app\_query.fasta\_1  
-DB=N\_Geneseq -QMT=fastcap -SUFFIX=ing -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORM=exc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h  
-USER=US10635908 @CCN\_1\_1\_942 @runat\_02062006\_104212\_10223 -NCPU=6 -ICPU=3  
-NO MMP -NEG SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_8.\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1030	92.3	717 6	AAD45759 Human CSE
2	1030	92.3	717 8	AB224023 Antibody
3	1021	91.5	717 2	At62929 Murine an

4	1021	91.5	5250 2	At62933	At62933 2A2 human
5	1017	91.1	714 2	At103363	At103363 Anti-IL-8
6	1017	91.1	714 2	At78570	At78570 Chimeric
7	1017	91.1	714 2	At93545	At93545 Chimeric
8	1017	91.1	714 2	AAV03206	AAV03206 Murine va
9	1017	91.1	714 2	AAV06413	AAV06413 Chimeric
10	1017	91.1	714 2	AAV55098	AAV55098 Anti-IL-8
11	1017	91.1	714 2	AAV10292	AAV10292 Mab 5.12.
12	1017	91.1	714 2	AAV90576	AAV90576 5.12.14 L
13	1017	91.1	714 3	AA287952	AA287952 Chimeric
14	1017	91.1	714 3	AA65491	AA65491 5-12-14 a
15	1017	91.1	714 8	ABX63872	ABX63872 Mouse ant
16	1017	91.1	714 8	ABX81399	ABX81399 Mouse ant
17	1017	91.1	714 10	AAV59293	AAV59293 Murine 5.
18	1014	90.9	642 14	AE85863	AE85863 Mouse OKT
19	1007	90.2	1701 14	AE18933	AE18933 Human mon
20	983	88.1	957 2	AA054654	AA054654 chITg4.12
21	977.5	87.6	699 14	AE28032	AE28032 Antibody
22	964	86.4	862 13	ADU68008	ADU68008 Mouse ant
23	964	86.4	862 14	AE041909	AE041909 Deimmuniz
24	964	86.4	12514 12	AD036181	AE138713 Monoclonal
25	961	86.1	714 15	AE38710	AE38710 Plasmid p
26	961	86.1	10103 15	AE38710	Adf77149 Chimeric
27	957	85.8	731 12	ADP77149	Adf77149 Chimeric
28	956	85.7	702 10	ACF57937	ACF57937 Humanised
29	956	85.7	702 10	ACF57939	ACF57939 Humanised
30	954.5	85.5	711 6	AA897086	AA897086 DNA encod
31	954.5	85.5	711 8	AA160501	AA160501 LM1 fusio
32	954.5	85.5	711 10	ADJ79819	Adj79819 LM2 DNA s
33	954	85.5	717 12	AD11351	Ad11351 BHA10 VL#
34	948	84.9	642 6	AA031362	AA031362 Antibody
35	948	84.9	642 12	ADH34231	ADH34231 Anti-huma
36	945	84.7	708 10	ADP93784	ADP93784 Monoclonal
37	945	84.7	748 2	AAQ23568	AAQ23568 Reshaped
38	945	84.7	12190 14	AE16286	AE16286 DNA sequ
39	944	84.6	662 14	ADX27043	ADX27043 Murine ht
40	943	84.2	968 4	AAH3873	AAH3873 Anti-HGF
41	939.5	84.1	2073 13	ADU23607	ADU23607 Human imm
42	939	84.1	2073 13	ADU23604	ADU23604 DNA vecto
43	938	84.1	1710 4	AA522533	AA522533 Human CDN
44	938	84.1	1710 4	AA522533	AA522533 Human CDN
45	938	84.1	1710 15	AAE23430	AAE23430 Novel hum

## ALIGNMENTS

RESULT 1	
AA045759	standard; DNA; 717 BP.
ID	AA045759; standard; DNA; 717 BP.
XX	
AC	AA045759;
XX	
DT	27-DEC-2002 (first entry)
XX	
DE	Human CSE10 antibody light chain DNA.
XX	
KW	Human; C49 antibody; C288 antibody; tumour associated antigen; TAG-72;
KW	neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
KW	non-Hodgkin's lymphoma; haematologic malignancy; tumour; gene; ds.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Location/Qualifiers
FT	1..717
FT	/tag= a
FT	/product= "Human CSE10 light chain protein"
XX	
PD	08-AUG-2002.
XX	
XX	W0200260955-A2.
XX	
XX	29-JAN-2002; 2002W0-US002373.





```
Db 373 GGGACCAAGCTGAAAATAAAGCACTGCTGCACCATCTCTTCACTTCCGCCA 432
Qy 121 SerAepGIUGLInLeuIysSerGIYThraIaSerValIaCysLeuLeuAnaPhenYr 140
Db 433 TCTGATGACAGCTGAAATCTGAACTGCCTCTGTGTGCTGCTGAATAACTTCTAT 492
Qy 141 ProAGGUAAlaIyValGInTrpIyValaAspAnaIaLeuGInSerGIYLeuSeriGIn 160
Db 493 CCCAGAGAGCCAAAGTACAGTGAAGGTGAATACGCCCTCCAAATGGGTAACCTCCAG 552
Qy 161 GluSerValThrGIUGInaSerIySaAspSerThrIYSerLeuSerSerThrLeuThr 180
Db 553 GAGAGTGTACACAGACGACGACCAAGACAGACCTTACAGCTTACGACACCCCGAGG 612
Qy 181 LeuSerLYaIaAspTYrGIuIySHiSlySvalTYraIaCysGIuValThrHISGInGIY 200
Db 613 CTGAGCAAGACAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCAACCATCAGGCG 672
Qy 201 LeuSerSerProValThrIySerPheAnaArgGIYGIuCYe 214
Db 673 CTGAGCTGCCCTCCACAAAGAGCTTCAACAGGGAGAGTGT 714

RESULT 4
ID AAT62933 standard; DNA; 5250 BP.
XX AAT62933;
AC AAT62933;
XX
DT 17-OCT-2003 (revised)
DT 16-JUN-1997 (first entry)
XX
DE 2A2 human IgG4 expression plasmid insert sequence.
XX
KW Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis; ss.
XX
OS Homo; sapiens.
OS Mus BP.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT exon 903..1055
FT FT /*tag= a
FT FT 1056..1285
FT FT /*tag= b
FT FT 1286..2020
FT FT /*tag= c
FT FT /codon_start= 1318
FT FT 2021..2410
FT FT /*tag= d
FT FT 2411..2446
FT FT /*tag= e
FT FT 2447..2564
FT FT /*tag= f
FT FT 2565..2894
FT FT /*tag= g
FT FT 2895..2991
FT FT /*tag= h
FT FT 2992..3314
FT FT /*tag= i
FT FT 3315..4045
FT FT /*tag= j
FT FT 4046..4198
FT FT /*tag= k
FT FT 4199..4428
FT FT /*tag= l
FT FT 4429..5177
FT FT /*tag= m
FT FT /codon_start= 4461
XX
XX MO9711971-A1.
```

```
PD 03-APR-1997.
XX
XX PF 27-SEP-1996; 96WO-US015575.
XX
XX PR 28-SEP-1995; 95US-0004489P.
XX PR 26-SEP-1996; 96US-0000489P.
XX
XX PA (ALEX-) ALEXION PHARM INC.
XX
XX PI Mueller JP, Evans WJ, Mueller EE, Rollins S, Rother RP, Matls LA,
XX WPI: 1997-212855/19.
XX DR P-PDB; AAW14935, AAW14936.
XX
XX PT Antibodies binding to porcine but not human cell interaction proteins -
XX PT useful to treat and assay for rejection of xenografted porcine organs,
XX PT tissues or cells.
XX
XX PS Disclosure; Page 47-52; 105pp; English.
XX
XX CC A DNA sequence (AAT62933) comprises a 2A2 human IgG4 expression plasmid
XX CC insert sequence. It is obcd. by cloning the light chain (see also
XX CC AAT62929) and heavy chain (see also AAT62930) variable region sequences
XX CC of murine anti-porcine vascular cell adhesion molecule (VCAM) monoclonal
XX CC antibody 2A2 into an expression plasmid modified to contain the human
XX CC gamma4 constant region in plasmid of the human gamma C1 region. The
XX CC encoded heavy chain (AAW14935) and light chain (AAW14936) can be used to
XX CC produce a chimeric antibody that is specific for porcine VCAM. The
XX CC chimeric antibody is useful for diagnosing human rejection of porcine
XX CC xenotransplants and for improving xenotransplantation of porcine cells,
XX CC tissues and organs into human recipients. (Updated on 17-OCT-2003 to
XX CC standardise OS field)
XX
XX SQ Sequence 5250 BP; 1236 A; 1469 C; 1352 G; 1193 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,27e-81 Length: 5250
Score: 1021.00 Matches: 194
Percent Similarity: 96.7% Conservative: 13
Best Local Similarity: 90.7% Mismatches: 7
Query Match: 91.5% Indels: 0
DB: Gaps: 2

US-10-635-908-15 (1-214) X AAT62933 (1-5250)
Qy 1 AepIleValMetThrGInSerGInaRgPheMetSerThrThValGIYAspArgValSer 20
Db 4533 GACATTGTGATGACCCAGTCTCAAAATTCATGTCCATCATYAGAGACAGGGGTCAAC 4592
Qy 21 IleThrCysAlaIaSerGInaAnaValaIaSerAlaValaIaTrpYrGInGInIyProAsp 40
Db 4593 GTACCTGCAAGGCCAGTCAAAATGTGGTCTCTTAATGTGCTGTTCACAGAAACCA 4652
Qy 41 GIYGIuSerProLYeLeuLeuIleTYrSerAlaIaSerAnaArgTYrThrGIYValProAsp 60
Db 4653 GGCAGATCTCCATAAACACTTATTACTCGCATCTTCGCTACAGTGAAGTCCCTGAT 4712
Qy 61 ArgPheThrGIYSerGIYSerGIYThraAspPheThrLeuThrIleSerAnaMetGInSer 80
Db 4713 CGCTTCACAGGACAGTGAATCTGGGACAGATTTCACCTCACATCAATGACAGTCT 4772
Qy 81 GluAepLeuAlaAspPheCysGInGInTYrSerAnaTYrProTrpThrPheGIYGIY 100
Db 4773 GAGAGCTTGACAGAGATTTCTGTCTCATATTAATCTTACCTTCTACGTTCCGGGGG 4832
Qy 101 GIYThrLYeLeuGIuIleLYaRgThraIaIaIaProSerValPheIlePhePro 120
Db 4833 GGGACCAAGCTGAAAATAAAGCAACTGTGCTGACCATCTGTCTTCACTTCCGCCCA 4892
Qy 121 SerAepGIUGLInLeuIysSerGIYThraIaSerValIaCysLeuLeuAnaPhenYr 140
Db 4893 TCTGATGACAGCTGAAATCTGAACTGCCTCTGTGTGCTGCTGAATAACTTCTAT 4952
```

QY 141 ProArgGluAlaIalysValGlnTrpIysValIAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
 DB 4953 CCCAGAGAGGCCAAAGTACAGTGAAGGATTAACGCCCTCAATCGGGTAATCTCCAG 5012  
 QY 161 GluSerValThrGluGlnAspSerIysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
 DB 5013 GAGAGTGTCAAGAGCAGACGACGACCAAGCCTACAGCCTCAGCAGCAGCCTGAGC 5072  
 QY 181 LeuSerIysAlaAspTyrGlnIulysHsIysValIYrAlaCysGluValThrHisGlnGly 200  
 DB 5073 CTGAGCAAAAGCAGACTACGAGAAACCAAAAGTCTACGCTGCGAGAGTCAACCATCAGGAC 5132  
 QY 201 LeuSerSerProValThrIysSerPheAsnArgGlyGluCys 214  
 DB 5133 CTGAGCTGCGCCCTCAACAAAGACTTCAACAGGGGAGAGTGT 5174  
 RESULT 5  
 AAT03363  
 ID AAT03363 standard; cDNA; 714 BP.  
 AC AAT03363;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 03-APR-1996 (first entry)  
 XX  
 DE Anti-IL-8 Mab 5.12.14 VL/human IgG1 CL cDNA.  
 XX  
 KM Monoclonal antibody 5.12.14; Mab; interleukin-8; IL-8; chimeric antibody;  
 KW Fab; antibody engineering; inflammation; inflammatory bowel disease;  
 KW ulcerative colitis; bacterial pneumonia; ds.  
 XX  
 OS Mus musculus.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..69  
 FT /\*tag= a  
 FT /product= "SITI signal peptide"  
 FT mat\_peptide 70..396  
 FT /\*tag= b  
 FT /product= "Murine 5.12.14 light chain variable region"  
 FT mat\_peptide 397..713  
 FT /\*tag= c  
 FT /product= "Human IgG1 light chain constant region"  
 XX  
 PN WO9523865-A1.  
 XX  
 PD 08-SEP-1995.  
 XX  
 PF 01-MAR-1995; 95MO-US002589.  
 XX  
 PR 03-MAR-1994; 94US-00205864.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PA (INDV ) UNIV INDIANA FOUND.  
 XX  
 PI Doersehuk CM, Fong S, Herbert CA, Kim KJ, Leong SR;  
 XX  
 DR WPI; 1995-320580/41.  
 DR P-PSDB; AAR86319.  
 XX  
 PT New anti-interleukin-8 monoclonal antibodies - useful for treating  
 PT inflammatory disorders, partic. ulcerative colitis, and bacterial  
 PT pneumonia.  
 XX  
 PS Example E; Fig 19; 114pp; English.  
 XX  
 CC A cDNA insert (AAT03363) in vector pAS1214VL, codes for the light chain  
 CC variable region of anti-human interleukin-8 mouse monoclonal antibody  
 CC 5.12.14 and human IgG1 light chain constant region. The cDNA was obtd. by  
 CC amplification of cDNA derived from 5.12.14-producing hybridoma cells  
 CC using primers (AAT03352-55) based on light chain sequences. It is used

CC with cDNA (AAT03364) coding for the heavy chain variable region in the  
 CC prodn. of anti-IL-8 mouse-human chimeric Fab. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1,556-81 Length: 714  
 Score: 1017.00 Matches: 194  
 Percent Similarity: 96.3% Conservative: 12  
 Best Local Similarity: 90.7% Mismatches: 8  
 Query Match: 91.1% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-635-908-15 (1-214) x AAT03363 (1-714)  
 QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20  
 DB 70 GATATGTCATATACACAGTCTCAAAATTCATATGTCACATCATGAGAGAGGCTCAGC 129  
 QY 21 IletHrCysAlaSerGlnAsnValIAspAlaValIAlaTyrGlnGlnIulysPro 40  
 DB 130 GTACCTGCAAGGCCAGTCAAGATGCGGTATTAATGATGCTGATCAAGAAACCA 189  
 QY 41 GlyGlnSerProIulysLeuLeuIletYrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
 DB 190 GGGCAATCTCTTAAGACACTGATTAATCTGATCTTACCGGTACAGTGAAGTCCCTGAT 249  
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80  
 DB 250 CGCTTCACAGGACAGTGGATCTGGACAGATTCATCTCACTCAATCCATGCCATGCGACTCT 309  
 QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIulysSerAsnIulysProTyrPheGlyGly 100  
 DB 310 GAAGACTTGGCAGACATATTTCTGTCGCAATATTAATCATCTCTCACAGTTCGCTCT 369  
 QY 101 GlyThrIysLeuGlnIulysArgThrValAlaAlaProSerValPheIlePheProPro 120  
 DB 370 GGGACCCAGCTGAGAGCTTGAAGAGCTGTGGCTGACCAATCTGTCTTCACTTCCGCGCA 429  
 QY 121 SerAspGluGlnLeuIulysSerGlyThrAlaSerValIAlaCysLeuLeuAsnAsnPheTyr 140  
 DB 430 TCTGATGAGAGATTGAATCTGGAATCTGCTTCTGTGTGTGCTGTAATTAATCTTAT 489  
 QY 141 ProArgGluAlaIalysValGlnTrpIysValIAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
 DB 490 CCCAGAGAGGCCAAAGTACAGTGAAGGTGATTAACGCCCTCAATCGGGTAATCTCCAG 549  
 QY 161 GluSerValThrGluGlnAspSerIysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
 DB 550 GAGAGTGTCAAGAGCAGACGACCAAGACGACCACTTACAGCCTCAGCAGCAGCCTGACG 609  
 QY 181 LeuSerIysAlaAspTyrGlnIulysHsIysValIYrAlaCysGluValThrHisGlnGly 200  
 DB 610 CTGAGCAAAAGCAGACTACGAGAAACCAAAAGTCTACGCTGCGAGAGTCAACCATCAGGAC 669  
 QY 201 LeuSerSerProValThrIysSerPheAsnArgGlyGluCys 214  
 DB 670 CTGAGCTGCGCCCTCAACAAAGACTTCAACAGGGGAGAGTGT 711  
 RESULT 6  
 AAT78570  
 ID AAT78570 standard; cDNA; 714 BP.  
 AC AAT78570;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 03-NOV-1997 (first entry)  
 XX  
 DE Chimeric monoclonal antibody light chain region encoding cDNA.  
 XX  
 KW Interleukin-8; IL-8; antagonist; anti-interleukin-8 antibody; asthma;  
 KW inflammatory disorder; neutrophil chemotaxis; elastase release;

KW		ischaemic reperfusion; ARDS; dermatitis; bacterial pneumonia;
XX		inflammatory bowel disease; mouse; human; ds.
OS	Mus musculus.	
OS	Homo sapiens.	
OS	Chimeric.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..714
FT		/+tag= a
FT	sig_peptide	/product= "Chimeric_monoclonal_antibody_light_chain"
FT		1..69
FT		/+tag= b
FT	misc_feature	70..396
FT		/+tag= c
FT		/label= Murine_5.12.14_variable_light_chain_region
FT	misc_feature	397..714
FT		/+tag= d
FT		/label= Human_IgG1_constant_light_chain_region
XX		
PN	WO9701354-A1.	
XX		
PD	16-JAN-1997.	
XX		
PF	26-JUN-1996; 96WO-US011033.	
XX		
PR	27-JUN-1995; 95US-00491334.	
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Hebert CA, Kabakoff RC, Moore MW;	
XX		
DR	WPI; 1997-118712/11.	
DR	P-PsDB; AAW23786.	
XX		
PT	Treating asthma by admin. of interleukin-8 antagonist - pref. an antibody	
PT	that inhibits binding of IL-8 to neutrophil(e), neutrophil chemotaxis and	
PT	elastase release.	
XX		
PS	Example F; Fig 19; 101pp; English.	
XX		
CC	Methods for treating asthma in mammals w/ich interleukin-8 (IL-8)	
CC	antagonists (anti-IL-8 antibodies) have been produced. Murine 5.12.14	
CC	monoclonal antibody is an anti-IL-8 antibody. The present sequence	
CC	encodes the murine 5.12.14 variable light chain region and the human IgG1	
CC	constant light chain region chimeric monoclonal antibody. Anti-IL-8	
CC	antibodies are especially used to treat or prevent allergic asthma in	
CC	humans. They inhibit: (a) neutrophil chemotaxis in response to IL-8; (b)	
CC	IL-8-mediated release of elastase from neutrophils and (c) binding of IL-	
CC	8 to neutrophils. Anti-IL-8 antibodies can be used to treat many other	
CC	inflammatory disorders, e.g. ischaemic reperfusion, ARDS, dermatitis,	
CC	particularly bacterial pneumonia and inflammatory bowel disease. (Updated	
CC	on 17-OCT-2003 to standardise OS field)	
XX		
Seq	Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;	
	Alignment Scores:	
	Pred. No.: 1.55e-81 Length: 714	
	Score: 1017.00 Matches: 194	
	Best Local Similarity: 96.3% Conservative: 12	
	Best Percent Similarity: 90.7% Mismatches: 8	
	Query Match: 91.1% Indels: 0	
	DB: 2 Gaps: 0	
US-10-635-908-15 (1-214) x AAT78570 (1-714)		
Oy	1 AAPLeValMeThrInGInSeRGIaRvPhMeTSeRThrThrVaIGIaSPARvAlSer 20	
Dd	70 GAATATGTCGTACGACAGTGCTCAAAATTATCATGTCCACATCAGTAAGSAGAAGGGTCAGC 129	
Oy	21 IIEThCyALeYALASerGIaenVAlSeRLaValAlAtPrTYrGIngInLySPRo 40	
Dd	130 GTCCACTCGAAGGCCAGTGAAGATGTGGGTAAATGTACCTGGTATCAACGAAAACA 189	

QY	41	GlyGlnSerProValLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp	60
Db	190	GGGCAATCTCCCTAAAGACATGATTACTGTCATCTTACCGGACAGTGGAGTCCCTGAT	243
QY	61	ArgPheThrGlySerGlySerGlyTyrAspPheThrLeuThrIleSerAsnMetGlnSer	80
Db	250	CGCTTCACAGGACGAGTGGATCTTGGACAGATTTCACTCTCACCATCATGACCATGTGCA	309
QY	81	GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrrPthrPheGlyGly	100
Db	310	GAAAGACTTGGCAGACTATTCTTCGTCAAGCAATATAACTATCTCTCTCAGTTCGGCT	365
QY	101	GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro	120
Db	370	GGGACCAAGCTGGAGCTTGAAAGAGCTGTGGCTGCACCATCTGTCTTCATCTTCCGCCA	423
QY	121	SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr	140
Db	430	TCTGATGAGCACTTGAAATCTGGAACCTGCTTCTGTGTGGCTGCTGTAATACTTCTAT	488
QY	141	ProArgGluAlaLysValGlnTrrPlyValAspAsnAlaLeuGlnSerGlyAsnSerGln	160
Db	490	CCCAAGAGGGCCAAAGTACGTGAGAGGTGGATAAAGCCCTCCAAATCGGGTAACTCCAG	548
QY	161	GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr	180
Db	550	GAGAGTGTACAGAGCAGACGAGACAGCAAGACAGCACTTACAGCTTCAGACACACCTTACG	609
QY	181	LeuSerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGluValThrHseGlnGly	200
Db	610	CTGAGCAAAAGCAGACTACAGAGAAACCAAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGC	668
QY	201	LeuSerSerProValThrLysSerPheAsnArgGlyGlnCys	214
Db	670	CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGAGAGAGTGT	711
RESULT 7			
AAT93545			
ID	AAT93545	standard; cDNA; 714 BP.	
XX	AC	AAT93545;	
XX	DT	17-OCT-2003 (revised)	
XX	DT	24-FEB-1998 (first entry)	
XX	DE	Chimeric monoclonal antibody 5.12.14 light chain encoding cDNA.	
XX	KW	murine light chain; 5.12.14; human interleukin-8; IL-8; anti IL-8;	
XX	KW	pneumonia; complementarity determining region; CDR; variable region;	
XX	KW	constant region; chimeric; pantIL-8.2; neutrophil chemotaxis; ds.	
XX	OS	Mus sp.	
XX	OS	Homo sapiens.	
XX	OS	Chimeric.	
XX	XX	Location/Qualifiers	
FT	Key	1..714	
FT	CDS	/tag= a	
FT	sig_peptide	1..69	
FT	FT	/tag= b	
FT	FT	/note= "signal peptide of STII"	
FT	mat_peptide	70..711	
FT	FT	/tag= c	
FT	FT	/note= "amino acids 24-132 are of murine variable light	
FT	FT	region and amino acids 133-237 are of human constant	
FT	FT	light region "	
XX	PN	US5677426-A.	
XX	PD	14-OCT-1997.	
XX	XX		

PF 01-MAR-1995; 95US-00398613.  
 XX 03-MAR-1994; 94US-00205864.  
 XX (GETH ) GENENTECH INC.  
 PA Kim KJ, Leong SR, Fong S, Hebert CA;  
 PI WPI: 1997-511926/47.  
 DR P-PSDB; AAW42319.  
 XX  
 XX Fragments of antibody to human interleukin-8 - comprising light and/or  
 PT heavy chain sequences; used to prevent interleukin-8 mediated neutrophil  
 PT chemotaxis.  
 XX  
 XX Disclosure; Fig 19; 63pp; English.  
 XX  
 XX This cDNA encodes for the chimeric Fab 5.12.14 which comprises of  
 CC complementarity determining regions (CDRs) of a light chain variable  
 CC region of the murine species and light chain constant region of the human  
 CC immunoglobulin IgG1. This chimeric Fab is used to construct a plasmid  
 CC pantiIL-8.2 which consists of murine-human variable/constant regions of  
 CC both the light and heavy chains of 5.12.14 by various standard  
 CC recombinant techniques. The recombinant human-murine chimeric Fab has  
 CC anti interleukin-8 (IL-8) activity and can inhibit the IL-8 binding to  
 CC human neutrophils. This anti IL-8 Fab is used to prevent interleukin-8  
 CC mediated neutrophil chemotaxis which is useful in the treatment of  
 CC ulcerative colitis and bacterial pneumonia. (Updated on 17-OCT-2003 to  
 CC standardise OS field)  
 XX  
 XX Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.55e-81 Length: 714  
 Score: 1017.00 Matches: 194  
 Percent Similarity: 96.3% Conservative: 12  
 Best Local Similarity: 90.7% Mismatches: 8  
 Query Match: 91.1% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-635-908-15 (1-214) x AAT93545 (1-714)  
 QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrValGlyAspArgValSer 20  
 DB 70 GAATTCCTCATGACACAGCTCTCAAAATTCATGCGCCACATCAGTAGAGAGAGGGGTACG 129  
 QY 21 IleThrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40  
 DB 130 GTACCTCGCAAGGCACTCAAGATGTGGTACTAATGTAGCTGTATCAACAGAAACCA 189  
 QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
 DB 190 GGGCAATCTCTTAAGACATGATTACTCGTACCTACCGGTACAGTAGAGATGCTCCGAT 249  
 QY 61 ArgPheThrGlySerGlySerGlyTyrAspPheThrIleSerAsnMetGlnSer 80  
 DB 250 CGCTTCACAGGCACTGATCTGGACAGATTTCCTCCTCACCATCAACCATGTCAGTCT 309  
 QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIleTyrSerAsnTyrProTyrPheGlyGly 100  
 DB 310 GAAGACTTGGCAGACTATTCTCTGACCAATATAATCTATCTCTCACCGTTCGGTCT 369  
 QY 101 GlyThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120  
 DB 370 GGGCAAGAGCTGAGGCTTGAAGAGCTGTGGCTCAGCATCTGTCTTCATCTCCGCA 429  
 QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAspPheTyr 140  
 DB 430 TCTGATGACAGCTTGAATCTGGAATCTCTCTGTGTGTGTCCTGCGAATTAATCTTCTAT 489  
 QY 141 ProArgGluAlaLysValGlnTyrLysValAlaAsnAlaLeuGlnSerGlyLysSerGln 160  
 DB 490 CCCAGAGAGGCCAAAGTACAGTCAAGTAGAGGTGATTAACGCCCTCAATCGGTAATCTCCAG 549

QY 161 GluSerValThrGlnAlaAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
 DB 550 GAGAGTGTACACAGACAGACAGACAGACAGACCTACAGCTCAGACAGACCTGACG 609  
 QY 181 LeuSerLysAlaAspTyrGluLysIleLysValTyrAlaCysGluValThrHisGlnGly 200  
 DB 610 CTGAGCCAAAGCACTACGAGAAACCAAGTCTACGCTTGCAGAGTCAACCATCAGGCG 669  
 QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214  
 DB 670 CTGAGCTGCCCTTCACAAAGAGCTTCAACAGGGGAGAGTGT 711  
 RESULT 8  
 AAV03206  
 ID AAV03206 standard; DNA; 714 BP.  
 AC AAV03206;  
 XX  
 XX 17-OCT-2003 (revised)  
 DT 15-APR-1998 (first entry)  
 XX  
 XX Murine variable and human IgG1 constant region light chain DNA.  
 DE  
 XX Light chain; heavy chain; monoclonal antibody; interleukin-8; IL-8;  
 KW inflammatory disorder; bacterial pneumonia; neutrophil chemotaxis;  
 KW anti IL-8 monoclonal antibody; IL-8 mediated elastase release;  
 KW Streptococcus pneumoniae; Escherichia coli; Pseudomonas aeruginosa;  
 KW ulcerative colitis; ds.  
 XX  
 XX Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH CDS 1..714  
 FT /\*tag= a  
 FT 1..395  
 FT /\*tag= c  
 FT /\*note= "encodes the variable light chain region of the  
 FT murine antibody 5.12.14"  
 FT sig\_peptide 1..69  
 FT /\*tag= b  
 FT misc\_feature 396..714  
 FT /\*tag= d  
 FT /\*note= "encodes the constant light chain region of human  
 FT IgG1"  
 FT  
 XX US5666070-A.  
 PN  
 XX 11-NOV-1997.  
 PD  
 XX 01-MAR-1995; 95US-00398612.  
 PF  
 XX 03-MAR-1994; 94US-00205864.  
 PR  
 XX (INDV ) UNIV INDIANA.  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Kim KJ, Doerschuk CM, Leong SR, Fong S, Hebert CA;  
 FI WPI: 1997-558085/51.  
 XX P-PSDB; AAW42319.  
 DR  
 XX  
 XX Treatment of bacterial pneumonia - with monoclonal antibody specific for  
 PT interleukin-8; inhibits lung inflammatory conditions.  
 PT  
 XX  
 XX Disclosure; Fig 19; 63pp; English.  
 PS  
 CC The present sequence depicts the coding sequence for murine monoclonal  
 CC antibody 5.12.14 light chain variable region and the human IgG1 light  
 CC chain constant region. The 5.12.14 antibody is a murine anti interleukin-  
 CC 8 (IL-8) IgG2a isotype. IL-8 is a neutrophil chemotactic peptide secreted

CC by a variety of cells in response to inflammatory mediators. IL-8 can  
 CC play an important role in the pathogenesis of inflammatory disorders such  
 CC as adult respiratory distress syndrome (ARDS), septic shock and multiple  
 CC organ failure. Treatment of bacterial pneumonia in a mammal comprises  
 CC administering an anti IL-8 monoclonal antibody, such as, e.g. humanised  
 CC 5.12.14, that binds human IL-8 with a Kd of 10<sup>-8</sup> to 10<sup>-11</sup> M, inhibits  
 CC neutrophil chemotaxis in response to IL-8, inhibits IL-8 mediated  
 CC elastase release by neutrophils and does not bind to C3a, beta-TG or  
 CC platelet factor 4. IL-8 specific monoclonal antibodies are especially for  
 CC treating pneumonia caused by Streptococcus pneumoniae, E. coli or  
 CC Pseudomonas aeruginosa in humans. The antibodies may also be used in the  
 CC treatment of ulcerative colitis and other inflammatory conditions.  
 CC (Updated on 17-Oct-2003 to standardise OS field)

XX SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	1,55e-81	Length:	714
Score:	1017.00	Matches:	194
Percent Similarity:	96.3%	Conservative:	12
Best Local Similarity:	90.7%	Mismatches:	8
Query Match:	91.1%	Indels:	0
DB:	2	Gaps:	0

US-10-635-908-15 (1-214) x AAV03206 (1-714)

QY 1 AappIlevalMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20  
 DB 70 GATATGTCATGACACAGTCTCAAAATTCATGTCACATCAGTAGAGACAGGGGTCAAC 129  
 QY 21 IletHrCValaValaSerGlnaValaValaSerValaValaTyrPyrGlnGlnIlyPro 40  
 DB 130 GTACCTGCAAGGCCAGTCAGATGTGGTACTTAATGACCTGGATATCAAGAAACCA 189  
 QY 41 GlynSerProlyLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
 DB 190 GGGCAATCTCTAAAGCAGTATTTACTGTCATCTTACCGGACAGTGAAGTCCCTGAT 249  
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80  
 DB 250 CCCTTCACAGGCGGTGATCTGGACAGATTCACCTCACATCCATGCGCATGTGCGAGTCT 309  
 QY 81 GIuAaPLeuAlaAaPhePheCysGlnGlnIlyTyrSerAsnTyrProThrPheGlyGly 100  
 DB 310 GAAGACTTGGACACATATTTCTGTCAGCAATATATATCTCTCACGTTCCGATCCT 369  
 QY 101 GlynThrLeuGlnIleTyrArgThrValAlaAlaProSerValPheIlePheProPro 120  
 DB 370 GGGACCAAGCTGAGCTTGGAGAGCTGTGGTGCACCATCTGCTTCACTTCCCGCA 429  
 QY 121 SerAspGlnGlnLeuIlySerGlyThrAlaSerValValCyleuLeuAsnAsnPheTyr 140  
 DB 430 TCTGATGACACAGTGAATCTGGAACCTGCTTGTGTGTGGCTGTGAATACTTCTCT 489  
 QY 141 ProArgGlnAlaIleValGlnTyrPlyValaAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
 DB 490 CCCAGAGAGGCCAAAGTACAGTGAAGTGAATACGCTCCAAATCGGGTAACTCCAG 549  
 QY 161 GIuSerValThrGlnGlnAspSerIlyAspSerThrTyrSerLeuSerSerThrLeuThr 180  
 DB 550 GAAGTGTCTACAGAGCAGACAGCAAGAGACAGCCTACAGCTCAGACAGCCTGAGC 609  
 QY 181 LeuSerIlyAlaAspTyrGlyIlyValaValaValaValaValaValaValaValaVala 200  
 DB 610 CTGAGCAAGACACACTACAGAAACAAAGTCTAGCCCTGCAAGTCAACCTACAGGCG 669  
 QY 201 LeuSerSerProValThrIlySerPheAsnArgGlyGlyCys 214  
 DB 670 CTGAGCTCCGCCCTTCACAAAGAGCTTCAACAGGGGAGAGTGT 711

RESULT 9  
 AAV06413  
 ID AAV06413 standard; DNA; 714 BP.

XX

AAV06413;

AC 17-OCT-2003 (revised)  
 DT 01-MAY-1998 (first entry)

DE Chimeric monoclonal antibody 5.12.14 light chain encoding DNA.

XX murine light chain; 5.12.14; human interleukin-8; IL-8; anti IL-8;  
 KW pneumonia; complementarity determining region; CDR; variable region;  
 KW constant region; chimeric; pantIL-8; ulcerative colitis; ds.

OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.

XX Key Location/Qualifiers

FT CDS 1..714

FT sig\_peptide 1..69

FT mat\_peptide 70..711

FT /note= "amino acids 24-132 are of murine variable light  
 FT region and amino acids 133-237 are of human constant  
 FT light region"

PN US5702946-A.

PD 30-DEC-1997.

PF 01-MAR-1995; 95US-00398611.

PR 03-MAR-1994; 94US-00205864.

PA (GENTH ) GENENTECH INC.

PI Kim KJ, Hebert CA, Leong SR, Doerschuk CM, Fong S;

DR WPI; 1998-076425/07.

PT P-PSDB; AAW33741.

PS Monoclonal antibody specific for interleukin-8 - used for treating IL-8  
 PT mediated inflammatory diseases, e.g. ulcerative colitis.

XX Disclosure; Fig 19; 63pp; English.

CC This DNA encodes for the chimeric Fab 5.12.14 which comprises of  
 CC complementarity determining regions (CDRs) of a light chain variable  
 CC region of the murine species and light chain constant region of the human  
 CC immunoglobulin IgG1. This chimeric Fab is used to construct a plasmid of  
 CC pantIL-8.2 which consists of murine-human variable/constant regions of  
 CC both the light and heavy chains of 5.12.14 by various standard  
 CC recombinant techniques. The recombinant human-murine chimeric Fab has  
 CC anti interleukin-8 (IL-8) activity and can inhibit the IL-8 binding to  
 CC human neutrophils. This anti IL-8 Fab can be used for diagnosis of  
 CC interleukin-8 mediated inflammatory diseases and in the treatment of  
 CC ulcerative colitis and bacterial pneumonia. (Updated on 17-Oct-2003 to  
 CC standardise OS field)

XX SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	1,55e-81	Length:	714
Score:	1017.00	Matches:	194
Percent Similarity:	96.3%	Conservative:	12
Best Local Similarity:	90.7%	Mismatches:	8
Query Match:	91.1%	Indels:	0
DB:	2	Gaps:	0

US-10-635-908-15 (1-214) x AAV06413 (1-714)





```
Db 190 GGGCAATCTCTTAAGCACTGATTTACTGTCTACTCCGTACAGTGGAGTCCCTGAT 249
Qy 61 ArgpHeThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAnMetGlnSer 80
Db 250 CCTTCACAGGAGGATGATCTGGAGACATTTCACTCTACCATCAGCATGTCAGTCT 309
Qy 81 GluAspLeuAlaAspPheCysGlnGlnIleTyrSerAsnTyrProTrpThrPheGlyGly 100
Db 310 GAAGACTTGCCAGACTATTCTGTCTGTCAGCAATATACATCATCTCTCACTCCGTCCT 369
Qy 101 GlyThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 370 GGGACCAACTGAGAGCTTGGAGAGCTGTGGCTGCACCATCTGTCTTCACTTCCGCCA 429
Qy 121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAnsnPheTyr 140
Db 430 TCTGATGACAGCAGTTGAATCTGCACTGCTTCTGTGTGTGCTGCTGTAATAACTTCTAT 489
Qy 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAnsnSerGln 160
Db 490 CCCAGAGAGGCCAAAGTACAGTGAAGGTGGATTAAGCCCTCCAAATCGGGTAACTCCAG 549
Qy 161 GluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db 550 GAGAGTGTACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 609
Qy 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGly 200
Db 610 CTGAGCAAAAGCAGACTACGAGAAACAAAGTCTACGCCCTGCGAAGTCAACCATCAGGCG 669
Qy 201 LeuSerSerProValThrLysSerPheAnsnArgGlyGluCys 214
Db 670 CTGAGCTCGCGCTCACAAAGAGCTTCAACAGGGGAGAGTGT 711

RESULT 11
AAV10292
ID AAV10292 standard; DNA; 714 BP.
AC AAV10292;
DC 03-JUN-1998 (first entry)
DE Mab 5.12.14 and human IgG1 construct light chain region DNA.
KW Monoclonal antibody; Mab 5.12.14; interleukin-8; IL-8; anti-IL-8; murine;
KW ulcerative colitis; immunotherapy; bacterial pneumonia; variable region;
KW treatment; light chain; heavy chain; neutrophil chemotaxis inhibitor;
KW human; IgG1; constant region; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..714
FT FT /*tag= a
FT FT #ig_peptide 1..69
FT FT /*tag= b 70..714
FT FT /*tag= c
FT FT /product= "5.12.14-IgG1 construct"
FT FT /note= "5.12.14 light chain variable region and human
FT FT IgG1 light chain constant region construct"
PN US5707622-A.
XX 13-JAN-1998.
XX
XX 01-MAR-1995; 95US-00396851.
XX
XX 03-MAR-1994; 94US-00205864.
XX
XX (GETH ) GENENTECH INC.
XX
XX Kim KJ, Leong SR, Fong S, Hebert CA;
XX PI
```

```
XX MPI, 1998-100296/09.
DR P-PSDB; AAW40122.
XX
XX Immunotherapy of ulcerative colitis - with monoclonal antibody specific
XX for interleukin-8.
XX
XX Example B; Fig 19; 63pp; English.
XX
XX This sequence encodes the murine 5.12.14 (anti-IL-8) monoclonal antibody
XX (Mab) light chain variable region and the human IgG1 light chain constant
XX region construct. This construct is used in a novel method for treating
XX ulcerative colitis which involves the administration of an anti-IL-8
XX monoclonal antibody capable of binding to human interleukin-8 (IL-8) with
XX a Kd of 10-8 to 10-11 M. This Mab also inhibits neutrophil chemotaxis in
XX response to IL-8, inhibits IL-8-mediated elastase release by neutrophils
XX and does not bind to C5a, beta -TG or platelet factor 4. The anti-IL-8
XX antibodies can also be used for the treatment of bacterial pneumonia
XX
XX Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.55e-81 Length: 714
XX Score: 1017.00 Matches: 194
XX Percent Similarity: 96.3% Conservative: 12
XX Best Local Similarity: 90.7% Mismatches: 8
XX Query Match: 91.1% Indels: 0
XX DB: Gaps: 2
XX
XX US-10-635-908-15 (1-214) x AAV10292 (1-714)
XX
Qy 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db 70 GATATGTCATATACAGTCTCAAAAATTCATGTCATCACTGAGAGAGAGAGAGAGAGAGAG 129
Qy 21 IleThrCysLysAlaSerGlnAsnValAlaSerAlaValAlaTrpTyrGlnGlnLysPro 40
Db 130 GTCACCTGCAAGCCAGCTAGATGGGTACTAATGTAGTCCGTGATCAACAGAAACCA 189
Qy 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAnsnArgTyrThrGlyValProAsp 60
Db 190 GGGCAATCTCTTAAGCACTGATTTACTGTCAGCAATATACATCATCTCTCACTCCGTCCT 249
Qy 61 ArgpHeThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAnMetGlnSer 80
Db 250 CGCTTACAGGAGGAGTGGATCTGGAGACATTTCACTCTACCATCAGCATGTCAGTCT 309
Qy 81 GluAspLeuAlaAspPheCysGlnGlnIleTyrSerAsnTyrProTrpThrPheGlyGly 100
Db 310 GAAGACTTGCCAGACTATTCTGTCTGTCAGCAATATACATCATCTCTCACTCCGTCCT 369
Qy 101 GlyThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 370 GGGACCAACTGAGAGCTTGGAGAGCTGTGGCTGCACCATCTGTCTTCACTTCCGCCA 429
Qy 121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAnsnPheTyr 140
Db 430 TCTGATGACAGCAGTTGAATCTGCACTGCTTCTGTGTGTGCTGCTGTAATAACTTCTAT 489
Qy 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAnsnSerGln 160
Db 490 CCCAGAGAGGCCAAAGTACAGTGAAGGTGGATTAAGCCCTCCAAATCGGGTAACTCCAG 549
Qy 161 GluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db 550 GAGAGTGTACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 609
Qy 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGly 200
Db 610 CTGAGCAAAAGCAGACTACGAGAAACAAAGTCTACGCCCTGCGAAGTCAACCATCAGGCG 669
Qy 201 LeuSerSerProValThrLysSerPheAnsnArgGlyGluCys 214
```

DB 670 CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGAGAGAGTGT 711

RESULT 12  
AA90576  
ID AAX90576 standard; DNA; 714 BP.  
XX  
XX AAX90576;  
XX  
DT 05-OCT-1999 (first entry)  
XX  
XX 5.12.14 L chain V region and human IgG1 L chain constant region DNA.  
DE  
XX  
XX  
XX Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;  
KM diagnosis; inflammatory disorder; conjugate; immunoglobulin;  
KM fusion protein; ss.  
XX  
XX Synthetic.  
OS Mus musculus.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..714  
FT /\*tag= a  
XX  
XX MO9937779-AI.  
XX  
XX 29-JUL-1999.  
XX  
XX 19-JAN-1999; 99MO-US001081.  
XX  
XX 22-JAN-1998; 98US-00012116.  
PR 20-FEB-1998; 98MO-US003337.  
PR 24-JUL-1998; 98US-00121952.  
PR 24-JUL-1998; 98US-00122513.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Heel V, Kouments I, Leong SJ, Presta LG, Shahrokh Z, Zapata GA;  
XX WPI; 1999-469134/39.  
DR P-PSDB; AAY29446.  
XX  
XX New conjugates of nonproteinaceous polymers with antibody fragments, used  
PT for treating inflammatory disorders.  
XX  
PS Disclosure; Fig 19; 360pp; English.  
XX  
XX The present invention describes a novel conjugate having one or more  
CC antibody fragments covalently attached to one or more nonproteinaceous  
CC polymer molecules, where the apparent size of the conjugate is at least  
CC about 500 kDa. Conjugates of antibody fragments which bind the human  
CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for  
CC treating inflammatory disorders e.g. acute lung injury, ischaemic  
CC reperfusion disorder, and autoimmune diseases. They can also be used for  
CC treating e.g. inflammatory skin diseases including psoriasis and atopic  
CC dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases.  
CC The conjugates can also be used as reagents in an animal model system for  
CC in vivo study of the biological functions of the antigen recognised by  
CC the conjugate. The present sequence encodes the 5.12.14 light chain  
CC variable region and the human IgG1 light chain constant region fusion  
CC protein from the present invention  
XX  
SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.55e-81 Length: 714  
Score: 1017.00 Matches: 194  
Percent Similarity: 96.3% Conservative: 12  
Best Local Similarity: 90.7% Mismatches: 8  
Query Match: 91.1% Indels: 0  
DB: 2 Gaps: 0  
US-10-635-908-15 (1-214) x AAX90576 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20  
DB 70 GATATCGTCATGACACAGCTCAAAAATTCATGTCACATCGTAGAGACGGGTCAAC 129  
QY 21 IleThrCysValAlaSerGlnAsnValValSerAlaValAlaTriPyrGlnIleLysPro 40  
DB 130 GTACCTGCAGGCGCAGATGAGATGGGTACTAATGTAGCCCTGGTATCAACGAAACCA 189  
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaAspAsnArgTyrThrGlyValProAsp 60  
DB 190 GGGCAATCTCCCAAGCACTGATTTACTGTCATCTCAACCGGATCGAGTGCCTGAT 249  
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80  
DB 250 CGCTTCACAGGACGTGATCTGGACAGATTCACCTCACCTCACATCGACATGTCAGTCT 309  
QY 81 GluAspLeuAlaAspPheCysGlnGlnIleTyrSerAsnTyrProThrThrPheGlyGly 100  
DB 310 GAAGACTGCGACAGACTATTCTGTCAACATATTAATCATCTATCTCAAGTTCCGATCCT 369  
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120  
DB 370 GGGACCAAGCTGAGAGCTTGAAGAGCTGGCTGCACCACTGTCTTCACTTCCGCCCA 429  
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140  
DB 430 TCTGATGACAGATGTAATCTGGAACCTGCTTGTGTGTGCTGCTGTAATACCTTCTAT 489  
QY 141 ProArgGlnAlaLysValGlnTyrPlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
DB 490 CCCAGAGAGGCCAAAGTACGTGAGAGTGAATAGCCCTTCCAAATCGGGTAACTCCAG 549  
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
DB 550 GAGAGTGTCAACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 609  
QY 181 LeuSerIleValAspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGly 200  
DB 610 CTGAGCAAGCAGACGACTACGAGAAACAAAGTCTACGCCCTGCGAAGTCAACCATCAGG 669  
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214  
DB 670 CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGAGAGAGTGT 711

RESULT 13  
AA287952  
ID AA287952 standard; DNA; 714 BP.  
XX  
XX AA287952;  
AC  
XX 15-SEP-2003 (revised)  
DT 06-JUN-2000 (first entry)  
XX  
XX Chimeric anti-IL-8 antibody light chain DNA sequence.  
DE  
XX Interleukin-8; IL-8; monoclonal antibody; Mab; anti-IL-8; 6G4.2.5Y1N35A;  
KM inflammatory disorder; adult respiratory distress syndrome; mouse;  
KM affinity purification; 5.12.14; ds.  
XX  
XX Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX  
XX US6025158-A.  
XX  
XX 15-FEB-2000.  
PD 20-FEB-1998; 98US-00027449.  
XX  
XX 21-FEB-1997; 97US-0038664P.  
PR 22-JAN-1998; 98US-0074330P.  
XX

PA (GETH ) GENENTECH INC.  
 XX Presta LG, Leong SR, Gonzalez TN;  
 XX WPI; 2000-181809/16.  
 DR P-PSDB; AAY77744.  
 XX  
 PT New nucleic acid molecule encodes a polypeptide which is an anti-  
 PT interleukin-8 monoclonal antibody or antibody fragment useful for the  
 PT production of anti-interleukin-8 monoclonal antibodies or fragments.  
 XX  
 PS Example; Fig 19; 188bp; English.  
 XX  
 CC The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody  
 CC (Mab). The anti-IL-8 Mab comprises a sequence containing the CDRs  
 CC (complementarity determining regions) of the humanized anti-IL-8  
 CC 6G4.2.5V11N35A light chain; and amino acids 24-253 of the humanized anti-  
 CC IL-8 6G4.2.5V11N35A heavy chain. The anti-IL-8 Mabs and fragments can be  
 CC used in diagnosis, for affinity purification of IL-8 from recombinant  
 CC cell culture or natural sources and for the treatment of inflammatory  
 CC disorders e.g. adult respiratory distress syndrome. Nucleic acids  
 CC encoding the anti-IL-8 Mab can be associated in a vector with another  
 CC gene encoding another protein or protein fragment to produce a fusion  
 CC protein which can make isolation and/or purification of the protein an  
 CC easier process. The present sequence represents the nucleotide sequence  
 CC of murine anti-IL-8 antibody 5.12.14 light chain variable region and the  
 CC human IgG1 light chain constant region. (Updated on 15-SEP-2003 to  
 CC standardise OS field)  
 CC  
 SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 1,55e-81 Length: 714  
 Score: 1017.00 Matches: 194  
 Percent Similarity: 96.3% Conservative: 12  
 Best Local Similarity: 90.7% Mismatches: 8  
 Query Match: 91.1% Indels: 0  
 DB: 3 Gaps: 0

US-10-635-908-15 (1-214) x AA287952 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20  
 DB 70 GATATGTCATGACACAGTCTCAAAATTCATCTCCACATCAGTAGAGACAGGCTCAG 129  
 QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnIlyPro 40  
 DB 130 GTCACCTGCAAGGCCAGTCAAGATGTGGTACTAATGTAGCCCTGGTATCAACGAAACCA 189  
 QY 41 GlyGlnSerProLysLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
 DB 190 GGGCAATCTCTTAAGCAGCATGATTACTCTCATCTCAGCGAGAGTGGAGTCCCTGAT 249  
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80  
 DB 250 CGCTTCACAGGAGCGATCTGGACACAGATTTCATCTCAACATCAGCATGTCAGTCT 309  
 QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100  
 DB 310 GAAGACTTGGCAACATATTCTGTGCAGCATATATCATCTCTCAACGTCGGTCCCT 369  
 QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120  
 DB 370 GGGACCAAGCTGAGCTTCAAGAGCTGTGGCTGCACCATCTCTTTCATCTCCGCCCA 429  
 QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140  
 DB 430 TCTGATGAGACAGTGAATCTGGAACCTGCTTGTGTGGCTGCTGGAATAACTCTTAT 489  
 QY 141 ProArgGlnAlaLysValGlnTrpLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
 DB 490 CCCAGAGAGGCCAAAGATACAGTGAAGTGAATACGCCCTCCCAATCGGGTAACTCCACG 549

QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
 DB 550 GAGAGTGTCAACAGACAGACAGACAGACAGACACTTACAGCTTACAGACACCTGACG 609  
 QY 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGly 200  
 DB 610 CTGAGCAAGAGCAGACTTACAGAGAACACAAAGCTACGCTCGGAGATCACCATCAGAGC 669  
 QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214  
 DB 670 CTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGAGAGATGT 711

RESULT 14  
 AAC65491  
 ID AAC65491 standard, DNA; 714 BP.  
 XX  
 AC AAC65491;  
 XX  
 DT 12-FEB-2001 (first entry)  
 XX  
 DE 5-12-14 antibody light chain V region coding sequence SEQ ID NO: 24.  
 XX  
 KW Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;  
 KW adult respiratory distress syndrome; multiple organ failure;  
 KW bacterial pneumonia; inflammatory bowel disease; de.  
 XX  
 OS Unidentified.  
 XX  
 PN US6133426-A.  
 XX  
 PD 17-OCT-2000.  
 XX  
 PF 20-FEB-1998; 98US-00026985.  
 XX  
 PR 21-FEB-1997; 97US-0038664P.  
 PR 22-JAN-1998; 98US-0074330P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Presta LG, Leong SR, Gonzalez TN;  
 XX  
 DR WPI; 2000-686027/67.  
 XX  
 PT Humanized anti-interleukin 8 monoclonal antibody variant useful for  
 PT creating inflammatory disorders, such as adult respiratory distress  
 PT syndrome, hypovolemic shock and ulcerative colitis.  
 XX  
 PS Disclosure; Col 143-144; 240pp; English.  
 XX  
 CC The present invention provides a number of humanised monoclonal anti-IL-8  
 CC antibodies which can be used in the diagnosis and treatment of  
 CC inflammatory disorders, including adult respiratory distress syndrome,  
 CC septic shock, multiple organ failure, bacterial pneumonia and  
 CC inflammatory bowel disease. The present sequence encodes one of the  
 CC antibodies of the invention  
 XX  
 SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 1,55e-81 Length: 714  
 Score: 1017.00 Matches: 194  
 Percent Similarity: 96.3% Conservative: 12  
 Best Local Similarity: 90.7% Mismatches: 8  
 Query Match: 91.1% Indels: 0  
 DB: 3 Gaps: 0

US-10-635-908-15 (1-214) x AAC65491 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20  
 DB 70 GATATGTCATGACACAGTCTCAAAATTCATCTCCACATCAGTAGAGACAGGCTCAG 129  
 QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnIlyPro 40

```

Db      130 GTACCTGCAAGGCGCATGAGATGTGGACTAATGAGCCGTGATCAACAGAAACCA 189
Qy      41 GYGINSerProlyseuLeuLeuIleYrSerAlaSerAsnArgYrThrGlyValProAsp 60
Db      190 GGGCAATCTCTTAACACATGATTTACTGTCATCTCAGCGAGACGTGAGTCCCTGAT 249
Qy      61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db      250 CGCTTACACAGCAGTGTGATCTGGAGACAGATTACCTCACCATCAGCCATGTGAGTCT 309
Qy      81 GluAspLeuAlaAspPhePheCysGlnGlnIYrSerAsnIYrProTyrPthrPheGlyGly 100
Db      310 GAAGACTTGCGACACATATTCTGTCCAGCATATTAACATCATCTCTCAGCTTCGGTCT 369
Qy      101 GYThrIYrLeuGluIleLeuValArgThrValAlaAlaProSerValPheIlePhePro 120
Db      370 GGGACCAAGCTGAGCTTCGAAAGCTGTGGCTGCACATCTGTTCATCTTCCGCCCA 429
Qy      121 SerAspGluGlnIleuYrSerGlyThrAlaSerValValCysIleuLeuAsnAspPheYr 140
Db      430 TCTGATGAGCAGATTGAATCTGGAATCTCTTCTGTGTGCTCTGATTAATCTTCTAT 489
Qy      141 ProArgGluAlaIleYrValGlnTyrValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db      490 CCCAGAGAGCGCAAGATGACGTGGAAGTGTGATACGCCCTCCATCGGGTAATCTCCAG 549
Qy      161 GluSerValThrGluGlnAspSerIYrAspSerThrYrSerIleuSerSerThrLeuThr 180
Db      550 GAGAGTGTCAAGGAGCAGACAGCAGACAGACACCTCAAGCCTCAGACACACCTGACG 609
Qy      181 LeuSerIYrAlaAspTyrGlyIYrGlySHIleYrValIYrAlaCysGluValIYrHiSGlnGly 200
Db      610 CTGAGCAAAAGCAGACTTCGAGAAACCAAAAGTCTACGCCCTCGCAAGTCAACCTCAGGCC 669
Qy      201 LeuSerSerProValThrIYrSerPheAsnArgIYrGlyCys 214
Db      670 CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGAGAGAGTGT 711
RESULT 15
ABX63872
ID      ABX63872 standard; DNA; 714 BP.
XX
AC      ABX63872;
XX
DT      25-FEB-2003 (first entry)
XX
DE      Mouse anti-IL-8 mAb 5.12.14 VL/human IgG1 light chain DNA.
XX
KW      Antibody; monoclonal antibody; 5.12.14; 664.2.5; interleukin-8; mAb;
KW      antiinflammatory; respiratory; acute lung injury; polyethylene glycol;
KW      PEG; lung injury; adult respiratory distress syndrome; ARDS; asthma;
KW      inflammatory disease; inflammatory bowel disease; psoriasis; sclerosis;
KW      ischaemic reperfusion disorder; stroke; multiple sclerosis; meningitis;
KW      osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis;
KW      alcoholic hepatitis; cystic fibrosis; ds; mouse; human.
XX
OS      Mus sp.
OS      Homo sapiens.
OS      Synthetic.
OS      Chimeric.
XX
PN      US6468532-B1.
XX
PD      22-OCT-2002.
XX
PF      20-JAN-1999; 99US-00234340.
XX
PR      22-JAN-1998; 98US-0074330P.
PR      20-FEB-1998; 98US-0075467P.
PR      24-JUL-1998; 98US-0094003P.
PR      24-JUL-1998; 98US-0094013P.
XX

```

```

PA      (GETH ) GENENTECH INC.
XX
XX      HseI V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
PI
XX      WPI: 2003-138230/13.
DR
XX      P-PSDB; AB013778.
XX
PT      Treating acute lung injury in mammal by administering to mammal a 500 kD
PT      conjugate comprising F(ab')2 antibody fragment that binds to human
PT      interleukin-8, covalently attached to one or two polyethylene glycol
PT      molecules.
XX
XX      Example D, Fig 19, 259pp; English.
XX
XX      The invention relates to treating acute lung injury in a mammal,
XX      comprising administering to the mammal an effective amount of a conjugate
XX      of a single antibody fragment covalently attached to 1 or 2 polyethylene
XX      glycol (PEG) molecules, where the antibody fragment is a F(ab')2
XX      comprising: (a) first chain that is either a light chain or a heavy chain
XX      ; (b) a first opposite chain that is either a heavy chain opposite the
XX      first light chain or a light chain opposite the first heavy chain; (c) a
XX      second chain that is either a light chain or a heavy chain; and (d) a
XX      second opposite chain that is either a heavy chain opposite the second
XX      light chain or a light chain opposite the second heavy chain; where every
XX      PEG molecule is covalently attached to a first cysteine residue in the
XX      first or second chain that would ordinarily form a disulphide bridge with
XX      a second cysteine residue in the first or second opposite chain, where
XX      the disulphide bridge is avoided by substitution of another amino acid
XX      residue for the second cysteine residue in the first or second opposite
XX      chain, where the F(ab')2 comprises an antigen binding site that binds to
XX      human interleukin-8 (IL-8), and where the apparent size of the conjugate
XX      is at least about 500 kD. The antigen binding sites may be derived from
XX      murine monoclonal antibodies 5.12.14 or 664.2.5. The method is useful for
XX      treating lung injury, including adult respiratory distress syndrome
XX      (ARDS) in a mammal and inflammatory diseases (such as asthma,
XX      inflammatory bowel disease, psoriasis and sclerosis), ischaemic
XX      reperfusion disorders, stroke, autoimmune disease (e.g. Rheumatoid
XX      osteoarthritis), septic shock, cystic fibrosis and many other diseases
XX      and disorders listed in the specification. The present sequence is a
XX      nucleic acid encoding a light or heavy chain variable region from one of
XX      the mouse interleukin-8 monoclonal antibodies fused to human IgG light or
XX      heavy chain sequences
XX
SQ      Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1.55e-81 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: 8 Gaps: 0
US-10-635-908-15 (1-214) x ABX63872 (1-714)
Qy      1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db      70 GATATCTCATGACACAGTCTCAAAATTCATGTCACATCAGTACGAGACAGGCTCAGC 129
Qy      21 IleThrCysIYrAlaSerGlnAsnValValSerAlaValAlaTyrPyrGlnGlnIYrPro 40
Db      130 GTCACTCGCAAGGCGCATCGAAGTGTGATTCATATATAGCTGTGATCAACACAAACCA 189
Qy      41 GYGINSerProlyseuLeuLeuIleYrSerAlaSerAsnArgYrThrGlyValProAsp 60
Db      190 GGGCAATCTCTTAACACATGATTTACTGTCATCTCAGCGAGACGTGAGTCCCTGAT 249
Qy      61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db      250 CGCTTACACAGCAGTGTGATCTGGAGACAGATTTCATCTCACCATCAGCCATGTGAGTCT 309
Qy      81 GluAspLeuAlaAspPhePheCysGlnGlnIYrSerAsnIYrProTyrPthrPheGlyGly 100

```

```
Db      310 GAAAGACTTGACAGACTATTTCGTGACGAAATATACATCTATCTCTCAGCTTCGATCCT 369
Qy      101 GYThrLysLeuGluLeuLysArgThrValAlaAlaProSerValPheIlePhePro 120
Db      370 GGGACCAAGCTGGAGCTGCGAAGAGCTGGCTGCACCATCTGTCTTCACTTCCGCCA 429
Qy      121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
Db      430 TCTGATGAGCAGCTTGAATCTGGAACCTGCTTGTGTGTGCTGCTGTAATAACTTCTAT 489
Qy      141 ProArgGluAlaLysValGlnTyrLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db      490 CCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATTAACGCCCTCCATCGGGTAACTCCCA 549
Qy      161 GluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db      550 GAGAGTGTCAACAGACAGGACAGCAAGACAGCACCCTACAGCCTCAGACACCTGACG 609
Qy      181 LeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200
Db      610 CTGAGCAAAAGCACTACGAAACACAAAGTCTACGCCCTGCGAAGTCAACCCATCAGGGC 669
Qy      201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
Db      670 CTGAGCTCGCCCTCTCAAAAGACTTCAACAGGGGAGAGTGT 711
```

Search completed: June 3, 2006, 04:12:54  
Job time : 708.553 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 04:13:15 ; Search time 5393.06 Seconds  
(without time 3328.373 Million cell updates/sec)

Title: US-10-635-908-15

Perfect score: 1116  
Sequence: 1 DIVTOSQRFMTTGVDRVS.....EYTHGLSSPVTKSFNRGSC 214

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=x1h  
-O=/abs/ABSWEB.spool/US10635908/runat\_02062006\_104216\_10273/app\_query.fasta\_1  
-DB=EST -OPMT=fastcap -SUFFIX=rest -MINMATCH=0.1 -LOOPCH=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h  
-USR=US10635908\_@CGN\_1\_1/986 -runat\_02062006\_104216\_10273 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_hc.\*  
7: gb\_est2.\*  
8: gb\_est7.\*  
9: gb\_est8.\*  
10: gb\_est9.\*  
11: gb\_gsa1.\*  
12: gb\_gsa2.\*  
13: gb\_gsa3.\*  
14: gb\_gsa4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	948	84.9	867	2	BG754732 602714301
2	944	84.6	856	2	BG758881 602713278
3	933.5	83.6	742	2	BG756519 602715662
4	932.5	83.6	903	3	BQ706785 AGENCOURT

5	932	83.5	810	4	CB956774
6	932	83.5	943	2	BF976230
7	931	83.4	964	3	BQ706786
8	928	83.2	774	4	BX336281
9	926	83.0	925	3	BQ707105
10	925	82.9	803	4	CB958596
11	924	82.8	716	2	BG755921
12	923	82.7	750	2	BG755394
13	923	82.7	854	2	BG755490
14	922	82.6	1017	3	BQ056652
15	922	82.6	1047	3	BQ059853
16	922	82.6	1047	3	BQ063090
17	922	82.6	1124	2	BQ055107
18	921.5	82.6	840	2	BG755327
19	921	82.5	849	2	BG745589
20	920.5	82.5	776	2	BG684027
21	919	82.3	947	2	BQ706698
22	918.5	82.3	962	2	BG745435
23	918	82.3	1019	3	BM914405
24	917.5	82.2	785	2	BM008264
25	917	82.2	815	2	BG759762
26	916	82.2	1048	3	BQ065573
27	915	82.1	875	2	BG685868
28	915	82.0	667	1	AV651251
29	914.5	81.9	744	2	BG686771
30	914.5	81.9	1041	3	BQ072483
31	914	81.9	793	4	CB956343
32	914	81.9	854	4	BX397739
33	914	81.9	901	2	B1518472
34	913	81.8	1065	3	BQ061622
35	911.5	81.7	729	2	BG685280
36	911	81.6	721	2	BG686441
37	911	81.6	727	2	BG684242
38	911	81.6	728	2	BG757337
39	910.5	81.6	1010	3	BQ711412
40	910	81.5	994	3	BQ711273
41	910	81.5	914	3	BQ707157
42	910	81.5	971	3	BQ706202
43	910	81.5	1013	3	BQ642324
44	909	81.5	1016	3	BQ065254
45	909	81.5	1018	3	BQ065739

#### ALIGNMENTS

RESULT 1  
BG754732  
LOCUS 867 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602714301F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4854409 5',  
mRNA sequence.  
ACCESSION BG754732  
VERSION BG754732.1 GI:14065385  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 867)  
REFERENCE NIH-MGC Http://mgi.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
plate: LNCM1702 row: a column: 02  
High quality sequence stop: 805.

FEATURES  
source

Location/Qualifiers  
1..867  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4854409"  
/issue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_48"  
/notes="Organ: B-cells; Vector: pOT7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected by Ling  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

## ORIGIN

Alignment Scores:  
Pred. No.: 2,766-99 Length: 867  
Score: 948.00 Matches: 179  
Percent Similarity: 93.0% Conservative: 19  
Best Local Similarity: 84.0% Mismatches: 15  
Query Match: 84.9% Indels: 0  
DB: 2 Gaps: 0  
US-10-635-908-15 (1-214) x BG754732 (1-867)

QY 2 IIEVALMERThrGlnSerGlnArgPheMetSerThrValGlyAspArgValSerIle 21  
DB 88 ATCCAGTGGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGAGTACACATC 147  
QY 22 ThrCylLeuAlaSerGlnSerValValSerAlaValAlaTrpTyrGlnGlnLysProGly 41  
DB 148 ACTTGGCCGGCAGTACAGGCGCATTAAGCATGCTTAGCCCTGGATCAGACGAACAGG 207  
QY 42 GlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAspArg 61  
DB 208 AAAGCTCTCAAGCTCTGATCTGATGCTCCAGCTTGGAAAGTGGGGCTTCAAG 267  
QY 62 PheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSerGlu 81  
DB 268 TTACAGGCGAGTGGATCTGGACAGATTTCATCTCACTCAGACGACCTGACGCTGAA 327  
QY 82 AspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 101  
DB 328 GATTTGGCAACTTATTAAGTCAACAGTTAATTAATTAACCTTCACCTTCGGCGAGG 387  
QY 102 ThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProSer 121  
DB 388 ACCAAGGTGAGATCAACAACGACTGCGTCACTGCTCTTCACTTCCCGCATCT 447  
QY 122 AspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAspPheTyrPro 141  
DB 448 GATGAGCAGTTGAATCTGAACTGCTCTGTTGTGCTGCTGTAATTAATCTTATCC 507  
QY 142 ArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 161  
DB 508 AGAGAGGCCAAGATGACGTGAAGGTGATTAACCCCTCAATCGGGTAACTCCAGAG 567  
QY 162 SerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuTrpLeu 181  
DB 568 AGGTGACAGAGACAGACAGCAAGACAGCACTTACGCTCAGACGACCTGACGCTG 627  
QY 182 SerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGlyLeu 201  
DB 628 AGCAAGCAACATCAAGAAACACAAAGTCTTACGCTTCGAATGATCACCATCAGGGCTG 687  
QY 202 SerSerProValThrLysSerPheAsnArgTyrGlnCys 214  
DB 688 AGCTCGCCGCTCAAAAGAGCTTCAACAGGAGAGAGTGT 726

## RESULT 2

BG758881

LOCUS

DEFINITION

BG758881

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

EST.

Mammalia; Euteleostomi;

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Euteleostomi; Euteleostomi; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 856)

NIH-MGC <http://mhc.nci.nih.gov/>.

AUTHORS

TITLE

JOURNAL

COMMENT

Email: [cgapdb-remail.nih.gov](mailto:cgapdb-remail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCML699 row: 1 column: 20

High quality sequence stop: 746.

## FEATURES

source

Location/Qualifiers

1..856

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4853539"

/issue\_type="primary B-cells from tonsils (cell line)"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_48"

/notes="Organ: B-cells; Vector: pOT7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

## ORIGIN

Alignment Scores:

Pred. No.: 7,926-99 Length: 856  
Score: 944.00 Matches: 180  
Percent Similarity: 91.1% Conservative: 15  
Best Local Similarity: 84.1% Mismatches: 19  
Query Match: 84.6% Indels: 0  
DB: 2 Gaps: 0  
US-10-635-908-15 (1-214) x BG758881 (1-856)

QY 1 ASPLEVALMERThrGlnSerGlnArgPheMetSerThrValGlyAspArgValSer 20  
DB 74 GACATCAGATGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGTACAGTACAG 133  
QY 21 IIEThrCylLeuAlaSerGlnSerValValSerAlaValAlaTrpTyrGlnGlnLysPro 40  
DB 134 ATCACTTGCAGCGCGAGTCAAGACATCAGCAACATTAATTAATTAATTAATTAATTA 193  
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
DB 194 GGGAAAGCCCTTAAAGTCTTAACTTCAATCATCTTAATTTGAAACAGGGGCTCCATCA 253  
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80



Db 254 AGGTCAGTGAAGTGGATCTGGGACAGATTTTACTTTCACCATCAGACCTGACGCT 313  
Qy 81 GUAAPLeuAlaasphephecysglnGlnTyrSerAsnTyrProThrPheGly 100  
Db 314 GAAGATCTTGACATCAATTAAGTCTCAACGATATGGCAATCTCCGCTTACTTTGGGGA 373  
Qy 101 GATThyLeuGlnTyrLeuArgThrValAlaAlaProSerValPheIlePhePro 120  
Db 374 GGGACCAAGTGGAGATCAACACAACTGGCTGACACCATCTGCTTCACTTCCGCCA 433  
Qy 121 SerAspGlnGlnLeuIleuysSerGlyThrAlaSerValValCysLeuLeuAsnAsn 140  
Db 434 TCTGATGAGCAGATTAATCTGAACTGCTCTGTTGTGTGCTGCTGATTAATCTTAT 493  
Qy 141 ProArgGlnAlaIleValGlnTyrPheValAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
Db 494 CCCAGAGAGGCCCAAGTACAGTGAAGTGAATTAACCTCCCAATCGGTAACCTCCAG 553  
Qy 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
Db 554 GAAGTGTCAAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 613  
Qy 181 LeuSerLysAlaAspTyrGlnTyrGlnTyrValTyrAlaCysGlnValThrIleGln 200  
Db 614 CTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCAACCCATCAGGGC 673  
Qy 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214  
Db 674 CTGAGCTCGCCCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT 715

RESULT 3  
Bg756519 742 bp mRNA linear EST 15-MAY-2001  
LOCUS DEFINITION 602715662F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4855839 5',  
mRNA sequence.  
Bg756519  
Bg756519.1 GI:14067172

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 742)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LNCMT05 row: 1 column: 16  
High quality sequence stop: 740.  
Location/Qualifiers

FEATURES  
source  
1..742

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_image="4855839"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGACACAG(G). Size selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald W. Rubin (University of

ORIGIN  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

Alignment Scores:  
Pred. No.: 1.08e-97 Length: 742  
Score: 933.50 Matches: 178  
Percent Similarity: 92.1% Conservative: 20  
Best Local Similarity: 82.8% Mismatches: 16  
Query Match: 83.6% Indels: 1  
DB: 2 Gaps: 1

US-10-635-908-15 (1-214) x Bg756519 (1-742)

Qy 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20  
Db 79 GACATCCAGATGACCCAGTCTCTTCCACCCGCTCGCATCTGTAGAGACAGATCACC 138  
Qy 21 ILeThrCysLysAlaSerGlnAsnValValSerAlaValAlaTyrPyrGlnIlePhePro 40  
Db 139 ATCACTTCCCGGCGCAGTCAAGATTAATTAAGCTGTGGCTTGGCTGTATCAGAGAACCA 198  
Qy 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
Db 199 GGGAAAGCCCTTAAGTCTCGATCTTAAGCCGCTTAAGTTAGAAAGTGGGGTCCCATCA 258  
Qy 61 ArgPheThrGlySerGlySerGlyTyrThrAspPheThrIleSerAsnMetGlnSer 80  
Db 259 AGGTTACGCGCGAGTGATCTGGACAGAAATTAATTAATTAATTAATTAATTAATTAAT 318  
Qy 81 GUAAPLeuAlaasphephecysglnGlnTyrSerAsnTyr---ProThrPheGly 99  
Db 319 GATGATTTTSCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 378  
Qy 100 GlyGlyThrLysLeuGlnTyrLeuArgThrValAlaAlaProSerValPheIlePhePro 119  
Db 379 CAAGGACCAAGGAGTGAATCAACGAACTGGCTGACACATCTGCTTCACTTCCG 438  
Qy 120 ProSerAspGlnGlnLeuIleuysSerGlyThrAlaSerValValCysLeuLeuAsnAsn 139  
Db 439 CCATCTGATAGACAGTTGAATCTGAACTGCACTGCTTGTGTGCTCGTGAATTAATCTTC 498  
Qy 140 TyrProArgGlnAlaIleValGlnTyrPheValAlaAspAsnAlaLeuGlnSerGlyAsnSer 159  
Db 499 TATCCAGAGAGGCCAAAGTACAGTGAAGTGAATTAACCCCTCAATCGGGTAATCTCC 558  
Qy 160 GlnGlnSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeu 179  
Db 559 CAGAGAGTGTCAAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 618  
Qy 180 ThrLeuSerLysAlaAspTyrGlnTyrGlnTyrValTyrAlaCysGlnValThrIleGln 199  
Db 619 ACGGTGAGCAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 678  
Qy 200 GlyLeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214  
Db 679 GGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 723

RESULT 4  
Bg706785 903 bp mRNA linear EST 16-JUL-2002  
LOCUS DEFINITION AGENCOURT 7977104 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6216052  
5', mRNA sequence.  
Bg706785  
Bg706785.1 GI:21845684

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE  
1 (bases 1 to 903)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L16M2385 row: P column: 05  
High quality sequence stop: 697.  
Location/Qualifiers

## FEATURES

source  
1. 903  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/db\_xref="IMAGE:6216052"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lb="NIH\_MGC\_113"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 1,86e-97 Length: 903  
Score: 932.50 Matches: 179  
Percent Similarity: 92.1% Conservative: 19  
Best Local Similarity: 83.3% Mismatches: 16  
Query Match: 83.6% Indels: 1  
DB: 3 Gaps: 1

US-10-635-908-15 (1-214) x BQ706785 (1-903)

```
QY 1 AapleValMeThrgInserGlnArgPheMetSerThrThyValGlyAspArgValSer 20
   |||||
DB 65 GACATCAATGATGACCAAGTCTCCTCTGTCGTCATCTTACAGACAGAGATCACC 124
QY 21 IlerhCysLysAlaSerGlnAsnValValSerAla---ValAlaTrpTyrGlnGlnLys 39
   |||||
DB 125 ATCACTTTCGGCGAGTCAAGGTATTAGCAGCAGCTGGTACCTGATATCAGAGAAA 184
QY 40 ProGlyInSerProLysLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValPro 59
   |||||
DB 185 CCAGGGAAGCCCTTAACCTCGATCTATGTCATCCAGTTGCAAGTGGGGTCCCA 244
QY 60 AspArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGln 79
   |||||
DB 245 TCAGATTTCAGCGGACGTGATCTGGAGACGATTTCACTCTCACTACAGACCCGCGAG 304
QY 80 SerGluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGly 99
   |||||
DB 305 CCGAAGATTTCGCACTTCTTTTGTCAACAGATTCCAGATTCCCTCCAGACTTTCGGC 364
QY 100 GlyGlyThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePhePro 119
   |||||
DB 365 GAGGAGCAAGGTGAGATCAACAGACGTGGTGCACCACTGCTTCATCTCCCG 424
QY 120 ProSerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAspHe 139
   |||||
DB 425 CCATTCGATGAGACGATTGAATCTGGAACGCTCTGTTGTGCTCGCTGGAATTACTTC 484
QY 140 TyrProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSer 159
   |||||
DB 485 TATCCAGAGAGCCCAAGTACAGTGAAGTGAATTAACCCCTCCATCGGGTAACTCC 544
```

```
QY 160 GlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerThrLeu 179
   |||||
DB 545 CAGGAGAGTGTACAGAGACGAGCAAGGACAGACACTTACAGCTTCAGCAGACCTCG 604
QY 180 ThrLeuSerLysAlaAspTyrGluLysIleLysValTyrAlaCysGluValThrIleGln 199
   |||||
DB 605 AGCGTAGCAAGACAGACTACGAGAAACCAAGTCTACGCTGCGAAGTCAACCATCAG 664
QY 200 GlyLeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
   |||||
DB 665 GGCCTGAGCTCCGCCGTCAAAAGAGCTTCAACAGGGAGAGTGT 709
```

## RESULT 5

CB956774 810 bp mRNA 1linear EST 29-APR-2003  
LOCUS AGENCOURT.13666961 NIH\_MGC.184 Homo sapiens CDNA clone  
DEFINITION IMAGE:30353409 5', mRNA sequence.

ACCESSION CB956774  
VERSION CB956774.1 GI:30212891

KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

REFERENCE  
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
CDNA Library Preparation: CLOUTCH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: NDCM154 row: b column: 10  
High quality sequence stop: 607.  
Location/Qualifiers

## FEATURES

## source

1. 810  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/db\_xref="IMAGE:30353409"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_1lb="NIH\_MGC\_184"  
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgctggcc); Library is oligo-dT primed and directionally cloned. CDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGCCGATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 1,83e-97 Length: 810  
Score: 932.00 Matches: 178  
Percent Similarity: 92.5% Conservative: 20  
Best Local Similarity: 83.2% Mismatches: 16  
Query Match: 83.5% Indels: 0  
DB: 4 Gaps: 0

US-10-635-908-15 (1-214) x CB956774 (1-810)

```
QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db 108 GAAATGATGATGACGAGTCTCCAGGACACCTCTCTGTGTCTCCAGGGGAAAGATCCAC 167
QY 21 IleThrCysLeuValAspSerGlnValSerValValAlaIleThrPyrGlnGlnIlePro 40
Db 168 CTCCTCTGACGGGCGAGTCAAGATGTTAAACAACACTACTGAGCCGTGATCCAGCGAAGAACCT 227
QY 41 GlyGlnSerProIleLeuLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIle 60
Db 228 GGCAGAGCTCCCGAGCTCTCATCTATGTCATCCGCCAGGGGCACTGGTGTCTCAAC 287
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 288 AGGTTACAGTGGCGATGGGTCTGGGACAGATTCACTCTCACTCAACGACGCTCGAGTCT 347
QY 81 GluAspLeuAlaAspPheCysGlnGlnIleIleIleIleIleIleIleIleIleIleIleIle 100
Db 348 GAGGATTTTGCAGTTATTACTGTCAAGATATGAATAATGGCGCTCGAGCTCGGCA 407
QY 101 GlyThrIleLeuGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 120
Db 408 GGGACCAAGGTGAGATCAAAACAGCTGGCTGCACATCTGTCTTCACTTCCGCCCA 467
QY 121 SerAspGlnGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIle 140
Db 468 TCTGATGAGCATGTTGAATCTGAACTGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTAT 527
QY 141 ProArgGlnAlaIleValGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIle 160
Db 528 CCCAGAGAGCCCAAGATCAAGTGAAGTGAATTAACCCCTCAATGGGTAACTCCACG 587
QY 161 GluSerValThrGlnGlnAspSerIleAspSerThrIleIleIleIleIleIleIleIle 180
Db 588 GAGAGTGTCAAGAGCGAGGACAGCAAGACAGCACTTCAAGCTCCAGCAGACCTCAGC 647
QY 181 LeuSerIleValIleAspIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
Db 648 CTGAGCAAGCAGACTCTCGAGAAACAAAGTCTACCCCTCGGAAAGTCAACCCATCAGGGC 707
QY 201 LeuSerSerProValThrIleSerPheAsnArgGlyGlyCys 214
Db 708 CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 749
RESULT 6 943 bp mRNA linear EST 22-JAN-2001
LOCUS BF976230
DEFINITION 602245105F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336225 5',
mRNA sequence.
ACCESSION BF976230
VERSION BF976230
KEYWORDS BF976230.1 GI:12343445
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo
1 (bases 1 to 943)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rudin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L10C1208 row: 1 column: 02
High quality sequence stop: 721.
```

```
FEATURES
source
Location/Qualifiers
1..943
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4336225"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_note="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
```

ALIGNMENT SCORES:

Pred. No.:	Length:	Score:
2,266-97	943	932.00
Percent Similarity:	Matches:	92.1%
Best Local Similarity:	Conservative:	19
Query Match:	Mismatches:	17
DB:	Indels:	0
	Gaps:	0

US-10-635-908-15 (1-214) x BF976230 (1-943)

```
QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db 84 GACATCCAGATGACCCAGTCTCATCTCCGTCGTGATCTGTAGAGACAGAGTACAC 143
QY 21 IleThrCysLeuValAspSerGlnValSerValValAlaIleThrPyrGlnGlnIlePro 40
Db 144 ATCACTTGTGCGGCGAGTCAAGGATATTAGACAGCTGTTACCTCGTATCAGCAAGAACCA 203
QY 41 GlyGlnSerProIleLeuLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIle 60
Db 204 GGGAAAGCCCTTAAGCTCTGATCTATGTCATCCAGTTTGCAAACTGGGGTCCCATCA 263
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrIleuThrIleSerAsnMetGlnSer 80
Db 264 AGGTTCAAGCGGCGATGATCTGGACAGATTTCATCTCAACATCAGCAGACCTCAGCCT 323
QY 81 GluAspLeuAlaAspPheCysGlnGlnIleIleIleIleIleIleIleIleIleIleIleIle 100
Db 81 GAGGATTTTGCAGTTACTTATTTGTCAACAGGCTTAACAGTTTGGCCAG 383
QY 101 GlyThrIleLeuGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 120
Db 324 GAGGATTTTGCAGTTACTTATTTGTCAACAGGCTTAACAGTTTGGCCAG 383
QY 121 SerAspGlnGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIle 140
Db 384 GGGACCAAGCTGAGATCAAAACAGCTGGCTGCACATCTGTCTTCACTTCCGCCCA 443
QY 141 ProArgGlnAlaIleValGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIle 160
Db 444 TCTGATGAGCATGTTGAATCTGAACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAT 503
QY 161 GluSerValThrGlnGlnAspSerIleAspSerThrIleIleIleIleIleIleIleIle 180
Db 504 CCCAGAGAGCCCAAGTACAGTGAAGGTGATTAACCCCTCCATGGGGTAACTCCACG 563
QY 181 LeuSerIleValIleAspIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
Db 564 GAGAGTGTCAAGAGCGAGCAGACAGACAGACAGCCTTCAAGCTCCAGCAGCAGCCTGACG 623
QY 201 LeuSerSerProValThrIleSerPheAsnArgGlyGlyCys 214
Db 624 CTGAGCAAGCAGCTCTCGAGAAACAAAGTCTTCAAGCTTCAAGCTCAACCCATCAGGGC 683
QY 201 LeuSerSerProValThrIleSerPheAsnArgGlyGlyCys 214
Db 684 CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 725
```

RESULT 7  
 BQ706786 964 bp mRNA linear EST 16-JUL-2002  
 LOCUS BQ706786  
 DEFINITION AGENCOURT 7976126 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6214887  
 5' UTR sequence.  
 ACCESSION BQ706786  
 VERSION BQ706786.1 GI:21845685  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 964)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: Dr. Mark Watson  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1CM2382 row: 0 column: 16  
 High quality sequence stop: 659.  
 Location/Qualifiers  
 1.964  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6214887"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1ib="NIH MGC\_113"  
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGACAGAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.05e-97 Length: 964  
 Score: 931.00 Matches: 176  
 Percent Similarity: 91.1% Conservative: 19  
 Best Local Similarity: 82.2% Mismatches: 19  
 Query Match: 83.4% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-635-908-15 (1-214) x BQ706786 (1-964)  
 QY 1 AaPileValmEThrGlnSerGlnArgpMetSerThrThrValGlyAspArgValSer 20  
 Db 81 GACATCCAGATGACCCAGCTCCATCCCTGTCATCTGATAGAGACAGAAATCACC 140  
 QY 21 ILeThCyAluValAlaSerGlnaenValaSerAlaValaLalrPyTrGlnGlnlySPRO 40  
 Db 141 ATCACTTGGCGGCAAGTCAAGACATTAGCACTTTTAAATTGGTATCAGCAAGAACCA 200  
 QY 41 GlyGlnSerProlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60  
 Db 201 GGGAGAGCCCTTAATCTCTGATCTTACGATCCAGTTTGACAGTGGGGCCCATCA 260  
 QY 61 ArgpHeThrGlySerGlySerGlySerGlyThrAspPheThrLeuThrIleSerAnMetGlnSer 80  
 Db 261 AGGTCACGTGGAGTGGATCTGGAGACAGATTTCACCTCCACCATCAGAGTCTGCAACT 320

QY 81 GluAaPleuAlaAspPhePheCysGlnGlnIntyrsSerAenTyProTrpThrPheGlyGly 100  
 Db 321 GGAGATTTTGGCAACTACTCTGTCAACAGCTTAACAATACCCCTGGAGCGTCCGCCA 380  
 QY 101 GlyThrLyLeuGluGluLeuysArgThrValAlaAlaProSerValPheIlePheProPro 120  
 Db 381 GGGACCAAGGTGAATCAAGCAAGTGTGGTGCACATCTGTCTTACTCTCCGCCCA 440  
 QY 121 SerAaPglGlnLeuLySerGlyThrAlaSerValValCysLeuLeuAnAnPheTy 140  
 Db 441 TCTGATGACAGCTTAATAATCTGAACCTGCTGTGTGTGCTGTGTAATTAATCTTAT 500  
 QY 141 ProArgGluAlaLyValGlnTrpLyValaAspAnaAlaLeuGlnSerGlyAnSerGln 160  
 Db 501 CCCAGAGAGCCCAAGTACAGTGAAGGATACGAGGATACGCTCAATCGAGTAACTCCAG 560  
 QY 161 GluSerValThrGluGlnAspSerLyAspSerThrTySerLeuSerSerThrLeuThr 180  
 Db 561 GAGAGTGTACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 620  
 QY 181 LeuSerLyAlaAspTyGlyLyshiLyValTyAlaCysGluValThrIleGlnGly 200  
 Db 621 CTGAGCAAGCAGACTACAGAGAAACAAAGCTTACGCTGGAGATCACCATCAGGCG 680  
 QY 201 LeuSerSerProValThrLySerPheAenArgGlyGlyCys 214  
 Db 681 CTGAGCTGCGCCGTCACAAGAGCTTCAACAGGGAGAGTGT 722

RESULT 8  
 BX336281  
 LOCUS BX336281 774 bp mRNA linear EST 08-APR-2004  
 DEFINITION BX336281 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 Clone CS0D1026Y122 5-PRIME, mRNA sequence.  
 ACCESSION BX336281  
 VERSION BX336281.2 GI:46279255  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 774)  
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 JOURNAL On May 2, 2003 this sequence version replaced GI:30341499.  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1696.r

ORIGIN  
 Alignment Scores:  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?as=CS0D1026Y122P10Pic=1696.r.  
 FEATURES  
 source  
 1.774  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1026Y122"  
 /issue\_type="PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Pred. No.: 5,01e-97 Length: 774  
 Score: 928.00 Matches: 177  
 Percent Similarity: 92.1% Conservative: 20  
 Best Local Similarity: 82.7% Mismatches: 17  
 Query Match: 83.2% Indels: 0  
 DB: 4 Gaps: 0

US-10-635-908-15 (1-214) x BX336281 (1-774)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrValGlyAspArgValSer 20  
 DB 15 GACATCCAGATGACCCAGCTTCCTCATCTTCGATCTGATAGAGACAGAGTCACC 74  
 QY 21 IleThrCysLysAlaSerGlnAsnValAlaSerAlaValAlaIlePheGlnGlnPro 40  
 DB 75 ATCACTTGTGGCGAGTCAAGGATATTAGACGTGTGATCCCTGATTCAGCAAGAACCA 134  
 QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
 DB 135 GGGAAAGCCCTAAGCTCTGATCTATGCTGATCCATCCAGAAAGTGGGTCCTCATCA 194  
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrIleSerAsnMetGlnSer 80  
 DB 195 AGGTTACAGCGCGATGATCTGGACAGATTTCACTCTCCATCCAGACAGCTCCGACCT 254  
 QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTrpThrPheGly 100  
 DB 255 GAAGATTTTGCACCTTACTTGTCTCAACAGCTCAACAGTTCCCTCGAGAGTCGCCAA 314  
 QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaIleProSerValPheIlePhePro 120  
 DB 315 GGGACCAAGGTGAAATCAACAGAACTGGCTGCACATCTGCTTCATCTTCCGCCCA 374  
 QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnPheTyr 140  
 DB 375 TCTGATGAGCAGTTGAATCTGAACTGCTCTGTGTGTGCTCGAATTAATCTTAT 434  
 QY 141 ProArgGluAlaLysValGlnTyrLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
 DB 435 CCAGAGAGGCCCAAGTACAGTGAAGTGAATACCCCTCCATATGGGTACTCCAG 494  
 QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
 DB 495 GAGAGTGTCAAGAGCAGACAGACAGACAGACAGACAGCTCAACAGACAGCTCAGC 554  
 QY 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrTrpAlaCysGlnValThrHisGlnGly 200  
 DB 555 CTGGGCAAGCAGACTACAGAAACACAAAGTCTACCGCTGCCAAGTCAACCCATCAAGG 614  
 QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214  
 DB 615 CTGAGCTGCCCTGACAAAGCTTCAACAGGGAGAGTGT 656

RESULT 9 925 bp mRNA linear EST 16-JUL-2002  
 LOCUS B0707105  
 DEFINITION AGENCOURT\_8354630 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6281121  
 5', mRNA sequence.  
 ACCESSION B0707105.1 GI:21846004  
 VERSION B0707105  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 925)  
 REFERENCE NIH-MGC http://mgs.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cga@bbs-rcmail.nih.gov  
 Tissue Procurement: Dr. Mark Watson

FEATURES  
 source cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM2473 row: g column: 10  
 High quality sequence stop: 647.  
 Location/Qualifiers  
 1..925  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6281121"  
 /lab\_host="PH10B (phage-resistant)"  
 /clone\_1b="NIH MGC 113"  
 /note="Organ: spleen; Vector: pOTB7, Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCACAG(G). Library constructed by Ling Hong in the  
 Laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC Library."

#### ORIGIN

Alignment Scores:  
 Pred. No.: 1.1e-96 Length: 925  
 Score: 926.00 Matches: 176  
 Percent Similarity: 90.7% Conservative: 18  
 Best Local Similarity: 82.2% Mismatches: 20  
 Query Match: 83.0% Indels: 0  
 DB: 3 Gaps: 0

US-10-635-908-15 (1-214) x B0707105 (1-925)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrValGlyAspArgValSer 20  
 DB 71 GACATCCAGTGAACCAAGTCTCCATCTCTGCTGATTTGAGAGACAGATCACC 130  
 QY 21 IleThrCysLysAlaSerGlnAsnValAlaSerAlaValAlaIlePheGlnGlnPro 40  
 DB 131 ATCACTTGTGGCGAGTCAAGGATATTAGACGTGTGATCCCTGATTCAGCAAGAACCA 190  
 QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
 DB 191 GGGAAAGCCCTAAGCTCTGATCTGATCCATCTTGCACACTTGCACAAAGTGGGTCCTTCA 250  
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrIleThrIleSerAsnMetGlnSer 80  
 DB 251 AGGTTACAGCGCGAGTGAATGAAATTAATCACTTCAACAAACAGACAGCTCAGCT 310  
 QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTrpThrPheGly 100  
 DB 311 GAAGATTTTGCACCTTACTGTCAACAGTGAATTAATCCGTACACTTTGGCCAG 370  
 QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaIleProSerValPheIlePhePro 120  
 DB 371 GGGACTAAGCTGGAGATCAACAGAACTGGCTGCACATCTGCTTCATCTTCCGCCCA 430  
 QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnPheTyr 140  
 DB 431 TCTGATGAGCAGTTGAATCTGAACTGCTCTGTGTGTGCTCGAATTAATCTTAT 490  
 QY 141 ProArgGluAlaLysValGlnTyrLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
 DB 491 CCAGAGAGGCCCAAGTACAGTGAAGTGAATACCCCTCCATATGGGTACTCCAG 550  
 QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
 DB 551 GAGAGTGTCAAGAGCAGACAGACAGACAGACAGCTCAACAGCTCAGACAGACCTCAGC 610  
 QY 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrTrpAlaCysGlnValThrHisGlnGly 200

Db 611 CTGACCAAGACAGACTACGAGAAACCAAGTCTAGCCTGCGAAGTCCATCAGGCG 670

Qy 201 LeuSerSerProValThrLySerPheAenArgLyGluCys 214

Db 671 CTGAGCTGCCCGCTCCACAAAGAGCTTCAACAGGGGAGAGTGT 712

RESULT 10

CB958596 803 bp mRNA linear EST 29-APR-2003

LOCUS CB958596

DEFINITION AGENCOURT 1366622 NIH MGC 184 Homo sapiens cDNA clone

IMAGE:30354106 5', mRNA sequence.

CB958596

VERSION CB958596.1 GI:30214712

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 803)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

cDNA Library Preparation: Clontech Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.jhl.gov>

Plate: NDCM155 row: O column: 11

High quality sequence stop: 667.

Location/Qualifiers

1..803

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/lab\_host="DH10B (T1 phage-resistant)"

/clone="IMAGE:30354106"

/1ab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH MGC 184"

/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site\_1: S11 (ggccatctggcc); Site\_2: S11 (ggccgctggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCATTTATGCG-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

ORIGIN

Alignment Scores:

Prod. No.: 1,18e-96 Length: 803

Score: 928.00 Matches: 175

Percent Similarity: 91.6% Conservative: 21

Best Local Similarity: 81.8% Mismatches: 18

Query Match: 82.9% Indels: 0

DB: 4 Gaps: 0

US-10-635-908-15 (1-214) x CB958596 (1-803)

Qy 1 AepIleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20

Db 90 GACATCCAGTTGACCCAGTCCATCTCTCTGTCGACATCTAGAGAGACAGATCACC 149

Qy 21 IleThrCyselValAspSerGlnAenValValSerAlaValAlaIrrpTyrgInLysPro 40

Db 150 TTCACCTGCGGCGCCAGCTACAGCACTTAACAGTTATTAGCTGATACGAAACGCCA 209

Qy 41 GlyInSerProLyLeuLeuIleTySerAlaSerAenArgTyThrGlyAlaProAsp 60

Db 210 GGGAAAGCCCTTAAGCTCCTGATCTATGCTGATCCATTTTCCAAAGGGGATCCCATCA 269

Qy 61 ArgPheThrGlySerGlySerGlyThrAspPheThrIleuThrIleSerAenMetGlnSer 80

Db 270 AGTTTCAGCGGAGAGGATCCGAGACAGATTCACCTACAAATCAGCAGCGCTGACCT 329

Qy 81 GluAspLeuAlaAspPhePheCysGlnGlnTySerAenTyProTrpThrPheGlyGly 100

Db 330 GAAGATTTTGCAACTTATTACTGTCAACAACACTTAGCAATTAACCTCTCCTCCGCGGA 389

Qy 101 GlyThrLyLeuGluIleLySerArgThrValAlaAlaProSerValPheIlePhePro 120

Db 390 GGGACCCAGGTGACATCAACGAACGTGGCTGCACCACTGTCTTCACTTCCCGCCA 449

Qy 121 SerAspGluGlnLeuLySerGlyThrAlaSerValValCysLeuLeuAenPheTy 140

Db 450 TCTGATGACAGCTTGAATCTGAACTGCTCTGTGTGTGCTGTGAATTACTTCTAT 509

Qy 141 ProArgGluAlaLyValGlnTrpLyValAspAenAlaLeuGlnSerGlyAenSerGln 160

Db 510 CCCAGAGAGCCAAAGTACAGTGAAGGTGATTAACGCCCTCAATCGGTAACCTCCAG 569

Qy 161 GluSerValThrGluGlnAspSerLyAspSerThrTySerLeuSerSerThrLeuThr 180

Db 570 GAGAGTGTACAGAGAGAGAGACAGCAAGACACACCTACAGCTTCAGCAGCCTCGAGC 629

Qy 181 LeuSerLyAlaAspTyGluLySerHsLySerValTyAlaCysGlyValThrAspGlnGly 200

Db 630 CTGAGCAAGACAGACTACAGAAACCAAGTCTAGCCTGGGAAATCACCATCAGGCG 689

Qy 201 LeuSerSerProValThrLySerPheAenArgLyGluCys 214

Db 690 CTGAGCTGCCCGCTCCACAAAGAGCTTCAACAGGAGAGAGTGT 731

RESULT 11

BG755921 716 bp mRNA linear EST 15-MAY-2001

LOCUS BG755921

DEFINITION 602716389F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4856351 5',

RNA sequence.

CB955921

VERSION BG755921.1 GI:14066574

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 716)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.jhl.gov>

Plate: LNCM1707 row: A column: 24

High quality sequence stop: 714.

Location/Qualifiers

1..716

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4856351"

FEATURES

source

```

/tissue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH_MGC_48"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; DNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCACGACG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by ligation
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library."

```

## ORIGIN

Alignment Scores:	
Pred. No.:	1.33e-96
Score:	924.00
Percent Similarity:	89.7%
Best Local Similarity:	81.3%
Query Match:	82.8%
DB:	
Gaps:	2
Length:	716
Matches:	170
Conservative:	18
Mismatches:	22
Indels:	0
Gaps:	0

US-10-635-908-15 (1-214) X BG755921 (1-716)

Oy	1	AspIleValImeThrInSerGlnaArgPheMetSerThrThrValGlyAspArgValSer	20
Db	74	GACATCCGAAAGAACCCAGCTCTCTCCACCCCTGCTGCATCTATTCGGAGACAGAGTACC	133
Oy	21	IleThrCysValaSerGlnaAsnValaSerAlaValaIaIaIaPyrGlnGlnIlyAspPro	40
Db	134	ATCACTTCCCGGGCCAGTCAAGAAATATGTTCTTGCTGGCTGGTANACACAGAAACCA	193
Oy	41	GlyInSerProIysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp	60
Db	194	GGGAAAGGCCCTAACTCCTCATCTACATGAGGCTACTTAAACAATAAGGGGTCCCAAA	253
Oy	61	ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer	80
Db	254	AGGTTACACCGGACAGTGAGATCTGGGACAAATTCGCTCTCGCATCAGACCCCTACAGCTT	313
Oy	81	GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrThrPheGlyGly	100
Db	314	GATGATTTTGGCAACTTATTACTGCCAACAAATACATTTCTTATCGGTGACGTTGGCCAA	373
Oy	101	GlyThrIysLeuGlnIleIleYsArgThrValAlaIaIaProSerValPheIlePheProPro	120
Db	374	GGGACCGACGTGAGACATCAAGAGAACTGTGGCTGACACATCTGTCTATCTTCCCGCCA	433
Oy	121	SerAspGlnGlnLeuIlySerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr	140
Db	434	TCTGATGAGCACTTGAAATCTGGAACCTGCTGTGTTGTTGGCTCTGCTGAATACACTTCTAT	493
Oy	141	ProAlaArgGluAlaIlyValGlnTyrIysValaIaAspAsnAlaLeuGlnSerGlyAsnSerGln	160
Db	494	CCCAAGAGGCCCAAGTACAGTGAAGGTGAATACGCCCTTCATCGGGTAACTCCAG	553
Oy	161	GlnSerValaThrGlnGlnAspSerIysAspSerThrTyrSerLeuSerSerThrLeuThr	180
Db	554	GAGAGTGTACAGACAGACGACACGACAGACACCTACAGCTACAGACACCCCTGAGC	613
Oy	181	LeuSerIlysAlaAspTyrGlnIlyIysIlyValIyValaCysGlnValaThrHisGlnGly	200
Db	614	CTGAGCAAAAGCACTACAGAAACCAAAAGTCTAGCCTTGGAAGTCAACCATCAGAGC	673
Oy	201	LeuSerSerProValaThrIysSerPheAsnArgGlyGluCys	214
Db	674	CTGAGCTCCGCCGTCAAAAGAGCTTCAACAGGGAGAGGTGT	715

RESULT 12

LOCUS BGT55394

DEFINITION 6027133951F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4854133 5', mRNA sequence.

750 bp

mRNA linear

EST 15-MAY-2001

ACCESSION	BG755394
VERSION	BG755394.1
KEYWORDS	GI:14066047
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL	Hominidae; Homo.
COMMENT	1 (bases 1 to 750)
	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a>
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
	CDNA Library Preparation: Ling Hong/Rubin Laboratory
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LNLN at:
	<a href="http://image.lnl.gov">http://image.lnl.gov</a>
	Plate: L1CM1701 row: e column: 14
	High quality sequence stop: 711.
FEATURES	Location/Qualifiers

**Source**

```

1. .750
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:465413"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_48"
/clone_orig="B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI, cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

Alignment Scores:	
Pred. No.:	1,83e-96
Score:	923.00
Percent Similarity:	91.6%
Best Local Similarity:	80.8%
Query Match:	82.7%
DB:	
US-10-635-908-15 (1-214) x BG5755394 (1-750)	
	Length: 750
	Matches: 173
	Conservative: 23
	Mismatches: 18
	Indels: 0
	Gaps: 0

US-10-635-908-15 (1-214) x BG755394 (1-750)

QY 1 AsplIeIaMeCtThngInSeRcIaArpHeMeSeRtThrThVaIaGlyAspArgVaISeR 20  
 Db 66 GACATCCAGCGACCCAGCTCCCTCTTCCTGTCGATCTGTAAGAGACAGAGTACC 125  
 QY 21 ILeThrCyLySaIaSeRgInaSnVaIaSeRaIaVaIaIaTrPyGInGInLysPro 40  
 Db 126 GTCACTTCCGGGCGCAGTCAGGGCATTTAGTACTTTTAGCGCTGATACGCAAAACC 185  
 QY 41 GlyInSeRProLySLeuLeuILeYrSeRaIaSeRaAnagTyThnGlyVaIProAsp 60  
 Db 186 GGGAAAGCCCTTAACTCTGATCTAATCTGATCGCTTGGCAAAATGGGATCCATCA 245  
 QY 61 ArgPheThrGlySeRgIySeRcIyThraSpPheThrLeuThrIleSeRaSnMeCInSeR 80  
 Db 246 AGCTTCACGGCAGTGATCTGGGACAGATTCACTTCACAAATCAGCAGCTTCGAGCCT 305  
 QY 81 GluAspLeuAlaAspPhePheCysGInGInTyrSeRaAnTyRProTTrpPhrGheGlyI 100  
 Db 306 GAAGATTTCGCACTTAATTAAGTGTAGCAACTTAATTAAGTACCCTTTCACTTCCGCCCT 365





cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>

Plate: LNCM2054 row: c column: 02  
 High quality sequence start: 13  
 High quality sequence stop: 695.  
 Location/Qualifiers

## FEATURES

source

```
1..1017
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5809081"
/issue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_99"
/notes="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
```

## ORIGIN

## Alignment Scores:

Pred. No.: 3,66e-96 Length: 1017  
 Score: 922.00 Matches: 172  
 Percent Similarity: 90.7% Conservative: 22  
 Best Local Similarity: 80.4% Mismatches: 20  
 Query Match: 82.6% Indels: 0  
 DB: 3 Gaps: 0

US-10-635-908-15 (1-214) x BQ056652 (1-1017)

```
QY 1 AspIleValMetThrgInserGlnArgPheMetSerThrValGlyAspArgValSer 20
    |||||
DB 100 GACATCCAGATGACCCAGCTCTCTCCACCCCTGTCGATTGTAGAGACAGAAATCACC 159
    |||||
QY 21 IleThCylValAlaSerGlnAsnValAlaSerAlaValAlaTrrPyGlnGlnLysPro 40
    |||||
DB 160 ATACTTGGCCGGCCAGTCAAGATATTATTAACGTGGTCCCTGATCAACAAAACCA 219
    |||||
QY 41 GlyGlnSerProLysIleuLeuIleYrSerAlaSerAsnArgYrThrGlyValProAsp 60
    |||||
DB 220 GGGAGAGCCCCAAGCTCTGCTATTAAGCGCTATTAACAGGCGGCGTCCCATCA 279
    |||||
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrIleuThrIleSerAsnMetGlnSer 80
    |||||
DB 280 AGGTTGAGCGCGAGTGAATGAGACAGAAATTCAGTCAACATCAGACCTCGACGCT 339
    |||||
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIleYrSerAsnIleYrProTrrPheGlyGly 100
    |||||
DB 340 GAGGATTTTCCACATCTTAATCTGCCAAGATATCAAGATTAATTCGTGACCTTCGGCA 399
    |||||
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
    |||||
DB 400 GGGAGCAAGGTGAGATGAACGAACTGTGCTCCACATCTGCTTCATCTTCCCGCCA 459
    |||||
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
    |||||
DB 460 TCTGATGAGCAGTTGAATCTGGAATCTGCTGTTGTGCTGCTGAATTAATCTTAT 519
    |||||
QY 141 ProArgGlnAlaLysValGlnTrrLysValAspAsnAlaLeuGlnInserGlyAsnSerGln 160
    |||||
DB 520 CCCAGAGAGCCCAAGATGACAGTGAAGTGAATACCCCTCCCAATGGGGATCTCCAG 579
    |||||
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
    |||||
```

```
DB 580 GAGAGTGTCAACAGACAGACAGACAGACAGACAGACCTTACAGCTCAGCAGACCTGAGC 639
QY 181 LeuSerIlyAlaAspTyrGlyLysIlyValIYrAlaCysGlnValThrIseGlnGly 200
    |||||
DB 640 CTGACCAAGACGACTACAGAGAAACAAAGTCTACGCTGCGAAGTCAACCATCAGGCG 699
    |||||
QY 201 LeuSerSerProValThrIlySerPheAsnArgGlyGlnCys 214
    |||||
DB 700 CTGAGCTGCGCCGTCAACAAAGAGCTTCAACAGGAGGAGAGTGT 741
    |||||
```

## RESULT 15

BQ059853 1047 bp mRNA linear EST 29-MAR-2002  
 LOCUS  
 DEFINITION AGENCOURT 6793921 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5815984  
 5', mRNA sequence.

ACCESSION BQ059853  
 VERSION BQ059853.1 GI:19819193  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

REFERENCE 1 (bases 1 to 1047)  
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>  
 TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: Lou Staudt

cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>

Plate: LNCM2072 row: b column: 17  
 High quality sequence start: 23  
 High quality sequence stop: 711.  
 Location/Qualifiers

## FEATURES

source

```
1..1047
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5815984"
/issue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_99"
/notes="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
```

## ORIGIN

## Alignment Scores:

Pred. No.: 3,82e-96 Length: 1047  
 Score: 922.00 Matches: 172  
 Percent Similarity: 90.7% Conservative: 22  
 Best Local Similarity: 80.4% Mismatches: 20  
 Query Match: 82.6% Indels: 0  
 DB: 3 Gaps: 0

US-10-635-908-15 (1-214) x BQ059853 (1-1047)

```
QY 1 AspIleValMetThrgInserGlnArgPheMetSerThrValGlyAspArgValSer 20
    |||||
DB 115 GACATCCAGATGACCCAGCTCTCTCCACCCCTGTCGATTGTAGAGACAGAAATCACC 174
    |||||
```



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 06:47:11 ; Search time 213.357 Seconds  
(without alignments)  
2815.117 Million cell updates/sec

Title: US-10-635-908-15

Perfect score: 1116  
Sequence: 1 D1VMTQSGQFMSTVGDVRS.....EVTHQGLSPVTKSFNRGEC 214

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
	Ygapop 10.0	Ygapext 0.5
	Delpop 6.0	Delpext 7.0
	Delpop 6.0	Delpext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-Q=/abs/ABSSWEB.spool/US10635908/runat\_02062006\_104220\_10327/app.query.fasta\_1  
-DB=Issued\_Patents\_NA -OPMT=fasta -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.ccl  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abs902h -USER=US10635908 -SCEN 1.1.252 @runat\_02062006\_104220\_10327  
-NCPU=6 -ICPU=3 -NO MAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7

Database: Issued\_Patents\_NA.\*

1: /EMC\_Celerra\_SIDS3/prodata/2/ina/1.COMB.seq.\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/ina/5.COMB.seq.\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/ina/6.COMB.seq.\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/ina/65.COMB.seq.\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/ina/7.COMB.seq.\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/ina/7.COMB.seq.\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/ina/7.COMB.seq.\*  
8: /EMC\_Celerra\_SIDS3/prodata/2/ina/7.COMB.seq.\*  
9: /EMC\_Celerra\_SIDS3/prodata/2/ina/7.COMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/prodata/2/ina/backfillseq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	91.1	714	2	US-08-398-613A-27
2	1017	91.1	714	2	US-08-398-612A-27
3	1017	91.1	714	2	US-08-398-611A-27
4	1017	91.1	714	2	US-08-398-611A-27
5	1017	91.1	714	2	US-08-491-334A-27
6	1017	91.1	714	3	US-09-027-449-24
7	1017	91.1	714	3	US-08-804-444A-24
8	1017	91.1	714	3	US-09-026-985-24

9	1017	91.1	714	3	US-09-121-952A-24
10	1017	91.1	714	3	US-09-234-340A-24
11	1017	91.1	714	3	US-09-355-014-24
12	1017	91.1	714	5	US-09-726-258-24
13	948	84.9	642	5	US-09-875-221B-127
14	945	84.7	748	3	US-08-030-175-3
15	943	84.5	660	3	US-08-952-235-3
16	943	84.5	660	3	US-09-669-971-3
17	936	83.9	974	3	US-09-859-053-29
18	932	83.5	3819	3	US-09-042-353-393
19	932	83.5	3819	3	US-08-758-417A-243
20	931	83.4	1951	3	US-10-011-125A-1
21	931	83.4	3300	4	US-10-020-786-2
22	931	83.4	6072	3	US-08-908-469-99
23	930	83.3	2178	2	US-08-463-587A-24
24	930	83.3	2178	2	US-08-463-587A-24
25	930	83.3	2178	2	US-08-923-854-24
26	930	83.3	2178	7	PCT-US91-09133-25
27	929	83.2	714	3	US-09-472-087-62
28	928.5	83.2	4207	3	US-09-897-511A-7
29	928.5	83.2	5732	3	US-09-897-511A-6
30	928.5	83.2	9183	3	US-09-456-090A-45
31	928	83.2	672	3	US-09-453-234-45
32	928	83.2	672	2	US-08-467-420A-50
33	927	83.1	5703	2	US-08-470-110A-50
34	927	83.1	5703	2	US-08-667-769A-50
35	927	83.1	5703	2	US-08-940-371-50
36	927	83.1	5703	2	US-08-637-647-50
37	927	83.1	5703	3	US-10-700-740-50
38	927	83.1	5703	3	US-10-700-740-50
39	927	83.1	5703	7	PCT-US95-17082A-50
40	926	83.0	654	3	PCT-US96-13152-1
41	922.5	82.7	708	3	US-09-472-087-40
42	922.5	82.7	708	3	US-09-472-087-56
43	922.5	82.4	767	4	US-09-499-662-128
44	920	82.4	931	3	US-09-049-672A-19
45	918	82.3	705	2	US-08-488-376-16

#### ALIGNMENTS

RESULT 1  
US-08-398-613A-27  
; Sequence 27, Application US/08398613A  
; Patent No. 5677426  
GENERAL INFORMATION:  
APPLICANT: Fong, Sherman  
APPLICANT: Hebert, Caroline Alice  
APPLICANT: Kim, Kyung Jin  
APPLICANT: Leong, Steven R.  
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/398,613A  
FILING DATE: 01-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/205864  
FILING DATE: 03-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitts, Renee A.

```
/
/ REGISTRATION NUMBER: 35,136
/ REFERENCE/DOCKET NUMBER: 874P1-3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1489
/ TELEFAX: 415/952-9881
/ TELE: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-398-613A-27

Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: Gaps: 0

US-10-635-908-15 (1-214) x US-08-398-613A-27 (1-714)

QY 1 AaplleValMetThrcInserGlnArgPheMetSerThrThrValGlyAapArgValSer 20
DB 70 GATATGCTATGACACAGTCTCAAAATTCATGTCACATGAGAGACAGGCTCAGC 129
QY 21 ILeThrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 130 GTCACTGCAAGGCCAGTCAAGATGGGACTCAATGAGCCCTGGATCAACGAAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTTAAACACATGATTACTGCTCATCTTACCGGTACAGTGAAGTCCCTGAT 249
QY 61 ArgPheThrcGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTACAGGCGAGTGTGAGACAGATTACTCTCACCACAGCCAGTGCAGTCT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
DB 310 GAAGACTTGCCACAGATATTCTGTCAACATATACATGATCTCTCAGCTTCGCTT 369
QY 101 GlyThrLysLeuGlnIleLysAlaGthrValAlaAlaProSerValIleLeuPhePro 120
DB 370 GGGACCAAGCTGAGAGCTTCAAGAGCTGTGGCTGCAACATCTGCTTCACTTCCGCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAspPheTyr 140
DB 430 TCTGATGAGCAGTTGAAATCTGAACTGCTTCTGTGTGTGCTGCTGTAATTAATTCTAT 489
QY 141 ProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCCAGAGAGGCCAAAGATACAGTGAAGGTGATTAACGCCCTCAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGAGGTGTCAACAGAGGACAGCAAGGACAGCACTTACAGCTCAGCAGCAGCCGAGAG 609
QY 181 LeuSerLysAlaAspTyrGlyLysHISLysValTyrAlaCysGlnValThrIleGlnGly 200
DB 610 CTGAGCAAAAGCACTTACGAGAAACACAAAGCTTACGCTGCAAGTCAACCCATCAGGGC 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlnCys 214
DB 670 CTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGAGGAGAGTGT 711

RESULT 2
US-08-398-612A-27
/ Sequence 27, Application US/08398612A
/ Patent No. 5686070
/ GENERAL INFORMATION:
```

```
/
/ APPLICANT: Doershuk, Claire M.
/ APPLICANT: Fong, Sherman
/ APPLICANT: Hebert, Caroline Alice
/ APPLICANT: Kim, Kyung Jin
/ APPLICANT: Leong, Steven R.
/ TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
/ TITLE OF INVENTION: Treatment of Inflammatory Disorders
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/398,612A
/ FILING DATE: 01-MAR-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/398611
/ FILING DATE: 01-Mar-1995
/ APPLICATION NUMBER: 08/205864
/ FILING DATE: 03-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P0874P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-5530
/ TELEFAX: 415/952-9881
/ TELE: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Double
/ TOPOLOGY: Linear
/
US-08-398-612A-27

Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: Gaps: 0

US-10-635-908-15 (1-214) x US-08-398-612A-27 (1-714)

QY 1 AaplleValMetThrcInserGlnArgPheMetSerThrThrValGlyAapArgValSer 20
DB 70 GATATGCTATGACACAGTCTCAAAATTCATGTCACATGAGAGACAGGCTCAGC 129
QY 21 ILeThrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 130 GTCACTGCAAGGCCAGTCAAGATGGGACTCAATGAGCCCTGGATCAACGAAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTTAAACACATGATTACTGCTCATCTTACCGGTACAGTGAAGTCCCTGAT 249
QY 61 ArgPheThrcGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTACAGGCGAGTGTGAGACAGATTACTCTCACCACAGCCAGTGCAGTCT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
```

Db 310 GAAGACTTGACAGACTATTCTGTGACCAATATACATCTCTCAGTTCGGTCT 369  
Qy 101 GYThrLysLeuGluLileysaTgThrValAlaAlaProSerValPheIleProPro 120  
Db 370 GGGACCAAGCTGAGCTTGCAGAGAGTGGCTGCACCACTCTTCTTCCGCCCA 429  
Qy 121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAspPheTy 140  
Db 430 TCTGATGAGCAGTGAATGTGAATCTGTAATCTTCTGTGTGTGCTGTGTAATATCTTCT 489  
Qy 141 ProArgGluAlaLysValGlnTTPlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
Db 490 CCCAGAGAGGCCAAAGTACAGTGAAGTGAATAGCCCTCCCAATCGGGTAACTCCAG 549  
Qy 161 GluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
Db 550 GAGAGGTGTCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 609  
Qy 181 LeuSerLysAlaAspTyrGlyLysLysLysValTyrAlaCysGluValThrHisGlnGly 200  
Db 610 CTGAGCAAGCAGACCTACGAGAAACACAAAGTCTAGCCCTGGCAAGTCAACCCATCAGGCG 669  
Qy 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214  
Db 670 CTGAGCTCGCCCTCACAAGAGCTTCAACAGGGAGAGTGT 711

## RESULT 3

US-08-398-611A-27  
Sequence 27, Application US/08398611A  
Patent No. 5702946

## GENERAL INFORMATION:

APPLICANT: Doershuk, Claire M.  
APPLICANT: Fong, Sherman  
APPLICANT: Hebert, Caroline Alice  
APPLICANT: Kim, Kyung Jin  
APPLICANT: Leong, Steven R.  
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment  
TITLE OF INVENTION: Of Inflammatory Disorders  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/398,611A  
FILING DATE: 01-Mar-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/205864  
FILING DATE: 03-MAR-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P0874P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:  
LENGTH: 714 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
US-08-398-611A-27

## Alignment Scores:

Pred. No.: 1,866-112 Length: 714  
Score: 1017.00 Matches: 194  
Percent Similarity: 96.3% Conservative: 12  
Best Local Similarity: 90.7% Mismatches: 8  
Query Match: 91.1% Indels: 0  
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x US-08-398-611A-27 (1-714)

Qy 1 AsplleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20  
Db 70 GATATGTCATATGACACAGTCTCAAAATTCATGATCCATCATAGTAGAGACAGGCTCAGC 129  
Qy 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaAlaTrrPyrGlnGlnLysPro 40  
Db 130 GTCACCTGCAAGGCCAGTCAAGATGTGGTACATAGTATAGTCCGTATCAACAGAAACCA 189  
Qy 41 GlynSerProLysLeuLeuLileysaTgThrValAlaAlaProSerValPheIleProPro 60  
Db 190 GGGCAATCTCTTAAGCAGTATTTACTGTCTCTTACCTCAGCAGTGAAGTGAAGTCCGTAT 249  
Qy 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrLysSerAsnMetGlnSer 80  
Db 250 CGCTTCACAGGACAGTGAATCTGGAGACAGATTCTACCTCACATCCAGCAGTGCAGTCT 309  
Qy 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrrPThrPheGlyGly 100  
Db 310 GAAGACTTGACAGACTATTCTGTGACCAATATACATCTATCTCTCAGCTTCGGTCT 369  
Qy 101 GYThrLysLeuGluLileysaTgThrValAlaAlaProSerValPheIleProPro 120  
Db 370 GGGACCAAGCTGAGCTTGCAGAGAGTGGCTGCACCACTCTTCTTCACTTCCGCCCA 429  
Qy 121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAspPheTy 140  
Db 430 TCTGATGAGCAGTGAATGTGAATCTGTAATCTTCTGTGTGTGCTGTGTAATATCTTCT 489  
Qy 141 ProArgGluAlaLysValGlnTTPlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
Db 490 CCCAGAGAGGCCAAAGTACAGTGAAGTGAATAGCCCTCCCAATCGGGTAACTCCAG 549  
Qy 161 GluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
Db 550 GAGAGGTGTCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 609  
Qy 181 LeuSerLysAlaAspTyrGlyLysLysValTyrAlaCysGluValThrHisGlnGly 200  
Db 610 CTGAGCAAGCAGACCTACGAGAAACACAAAGTCTAGCCCTGGCAAGTCAACCCATCAGGCG 669  
Qy 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214  
Db 670 CTGAGCTCGCCCTCACAAGAGCTTCAACAGGGAGAGTGT 711

## RESULT 4

US-08-396-851A-27  
Sequence 27, Application US/08396851A  
Patent No. 5707622

## GENERAL INFORMATION:

APPLICANT: Fong, Sherman  
APPLICANT: Hebert, Caroline Alice  
APPLICANT: Kim, Kyung Jin  
APPLICANT: Leong, Steven R.  
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

```

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,851A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitch, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 874P1-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-396-851A-27

Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x US-08-396-851A-27 (1-714)
QY 1 Aspllevalmethrinserglnargphmetseththrvalgllyaspargvalser 20
DB 70 GATATGTCATGACACAGTCTCAAAATTCATGTCACATCAAGTACAGAGGTCACG 129
QY 21 IletHcYalysalaserGlnaenValIserAlaValAlatrptyrGlnGlnlyPro 40
DB 130 GTACCTGCAAGGCGACGTCAGATGCGGTACTAATGACCTGGATCAACAGAAACCA 189
QY 41 GylGlnserProlylsleuleuIetyrSerAlaserAsnArgTythrGlyValProasp 60
DB 190 GGGCATCTCTTAAAGACACTGATTTCGTCTATCTTACCGGTACAGTGGAGTCCCTGAT 249
QY 61 ArgpHeThrGlyserGlyserGlyThrappHeThrleuThrlIserasmetGlnser 80
DB 250 CGCTTCACAGGCGATGATCTGGACAGATTTCACCTCCACCATGCGACAGTCT 309
QY 81 GluaspLeuAlaaspHePheCysGlnGlnIntyrSerAsnTyProrHrPheGlyGly 100
DB 310 GAAGACTTGACACATATTTCTGTGACAAATATTAACATCTATCTTCACGTTCCGTCCT 369
QY 101 GlyThrllysleuGlnIlelyAsrGthrValAlaIalaproSerValPheIlePhePro 120
DB 370 GGGACCAAGCTGAGCTTGCAGAGCGTGGCGACCACTCTTCACTTCCCGCCA 429
QY 121 SerAspGlnGlnleuIySerGlyThrAlaserValValCysleuleuAsnAspHeTy 140
DB 430 TCTGATGACGAGTGAATCTGGAACGCTTCTGTGTGTGCTGCTGAATATCTTCTAT 489
QY 141 ProArGlnAlaIalysValGlnTrpIysValIaspAsnAlaIleuGlnserGlyAsnserGln 160
DB 490 CCCAGAGAGGCCAAAGTACAGTGAAGGTGATTAAGCCCTCCAAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGlnGlnAspSerIysAspSerThrTySerleuSerSerThrleuThr 180
DB 550 GAGAGTGTCAACAAGCAGACAGCAAGACAGCACTACAGCTTCAAGCAGCACTGAGC 609
```

```

QY 181 LeuSerIysAlaAspTyrgIulYehIlsyValTyraIaCysGlnuValThriGlnGly 200
DB 610 CTGAGCAAGCAGACGATCAGAGAAACAAAGTCTAGCGCTGGAGTCAACCATCAGGCG 669
QY 201 LeuSerSerProValThrlYsSerPheAsnArgIylGlyCys 214
DB 670 CTGAGCTGCCCGTCAACAAGAGCTTCAACAGGGAGAGACTGT 711

RESULT 5
US-08-491-334A-27
Sequence 27, Application US/08491334A
Patent No. 5874080
GENERAL INFORMATION:
APPLICANT: Hebert, Caroline A.
APPLICANT: Kabakoff, Rhona C.
APPLICANT: Moore, Mark W.
TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
Diseases and Asthma
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,334A
FILING DATE: 27-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
US-08-491-334A-27

Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x US-08-491-334A-27 (1-714)
QY 1 Aspllevalmethrinserglnargphmetseththrvalgllyaspargvalser 20
DB 70 GATATGTCATGACACAGTCTCAAAATTCATGTCACATCAAGTACAGAGGTCACG 129
QY 21 IletHcYalysalaserGlnaenValIserAlaValAlatrptyrGlnGlnlyPro 40
```

```

Ddb      ...::...
Qy       130 GTACCTCGAAGGCCCATGCAATGTGGTACTTAATTGAAGCCTGGATAACAAGAACC A 189
        41 GYGVNSerProLySLeuleuLefTySerAlaSeRnaMgTYrThrglyValProASP 60
Db      190 GGCCAAITCTCTMAAGCACATGATTNACTGCATCTCAACCGGATACAGAGTGAGTCCTGAT 249
Qy       61 ArgPheThrGIysSerGIysSerGLYTrhpAppHeIrrleuthrllesSerAsmMeGlInSer 80
Db      250 CGCTTCACAGSGAGTGATCTGGGACAGATTTCACCTTCACCTCACCATCAGCAGTGCAGACT 309
Qy       81 GlusApLeuMaLaaspHephecYGingIntYrSerAsnTYrProtyPrThrPhagIGLY 100
Db      310 GAAGACTTGSACACCTATTTCTGTCTGACGCAATTAACATCTATCTCTCAACGTTGGTICT 367
Qy       101 GLYTrhyLeueugLIulleYSarGrTHvalalaaIproSeRalpheIIePheProPro 120
Db      370 GGAACCAAAGTGGAGCTTCGAMAAGCTGTGGCTGACACATCTGTTCATCTTCCCCGCA 422
Qy       121 SerAPglunJlneulysserGIYThralaserValCYseLUenLuasnASphETyr 140
Db      430 TCTGATAGCAGATTGAATCTGGAACTGGAACCTGCTGTGTGTGCTGTCTGTAATTAACCTTCA 489
Qy       141 ProARGluMaLiaySaIgINTPLpySValaPaSnAIaleuGINserGIYAasnSerGln 160
Db      490 CCAGAGAGGSCAAAGTACAgTGGAAGGTGAATAACGCCCTTCANtCGGTPAACCTCCAG 549
Qy       161 GluseRalThrglugInasPeSerLySAspSerThryrSerLeuSerSerThIrleuthr 180
Db      550 GAGAGTCTCACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 609
Qy       181 LeuSERilyaLaapTYrGIuLySHislysaVAYraIAcyeGUivaIvThHisGIngLY 200
Db      610 CTGAGCAAAcAcAGACTPCAGAAACCAAAAGTCTACGCTCGGAAGTCAccCATCAGggCc 665
Qy       201 LeuSErSerProVALThryLSERIPheaNaArgLYGluCyE 214
Db      670 CTGAGCTCGCCCGCTCACAAAAGACTTCAcAGGGAgaGTgt 711

RESULT 6
US-09-027-449--24
; Sequence 24, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leonz, Steven R.
; APPLICANT: Preeta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-II-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
```

```

NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
US-09-027-449-24

Alignment Scores:
Pred. NO.: 1,86e-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: Gaps: 3

US-10-635-908-15 (1-214) x US-09-027-449-24 (1-714)

QY 1 AsplilevImetCtnrGlnSerGlnarGpHeMetSerThrValGlyAsparGValSer 20
DB 70 GATATCGTCATGACACAGCTCTCAAAAATTATGTCACATGCTAGTGGAGACGGGCTCAG 129
QY 21 lIethrCysLysAlaSerGlnAsnValISerAlaValAlaIlePTrGlnGlnLysPro 40
DB 130 GTCACTGTCAGAGGCCAGTCAGAAATGTGGGTACTATGTATGTCCTGGTATCAACAGAAACCA 189
QY 41 GlynInsrProLysLeuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
DB 190 GGGCATCTCTCTAAAGACATGATTACTGTCATCTCAACGGTACAGTGAAGTCCCTGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGGACGATGCGATCTGGGACAGATTCTCACTTCACCATCAGCCATGCGACGTCT 309
QY 81 GlusAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyPProTrpThrPheGlyGly 100
DB 310 GAAGACTTGGCAGACATATTCTGTGTCAGCAATATTAACATCTATCTCTCAGCTCGGTCTCT 369
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 370 GGGACCAAGCTGAGCTTCGAAAGACCTGTGGCTGCGCACCATCTGCTTCATCTTCCGCCCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThrIleAspSerValValCysLeuLeuAsnAsnPheTy 140
DB 430 TCTGATGTAGCAGCTTAAATCTGGAACTGCTTCTGTGTGTGCTGCTGTAATACCTTAT 489
QY 141 ProArgGlnAlaLysValGlnTrpLysValAlaAspAsnAlaLeuGlnInsrGlyAsnSerGln 166
DB 490 CCCAAGAGAGGCCAAAGTACAGTGAAGGTGATTAAGCCCTCCAAATCGGGTAACTCCAG 549
QY 161 GlnSerValThrGlnGlnAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 186
DB 550 GAGAGTGTCAACAGACAGACAGACAGCAAGACACACACTCAAGCTTCAGACAGACCTCGACG 609
QY 181 LeuSerLysAlaAspTyGlnLysHisLysValIleTyAlaCysGlnValThrHisGlnGly 200
DB 610 CTGACCAACAAGCAGACTTACGAGAACAACAAAGTCTTACGCTTGCAGAAAGTCAACCCATCAGGGC 665
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB 670 CTGAGCTCGCCCTGTCAACAAGAGCTTCAACAGGGGAGAGTGT 711

RESULT 7
US-08-804-444A-24
; Sequence 24, Application US/08804444A
; Patent No. 6,117,980
; GENERAL INFORMATION:

```

```

/ APPLICANT: Gonzalez, Tania N
/ APPLICANT: Leong, Steven R.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
/ NUMBER OF SEQUENCES: 61
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpatin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/804,444A
/ FILING DATE: 21-Feb-1997
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P1085
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/952-9881
/ TELEFAX: 650/225-5530
/
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Double
/ TOPOLOGY: Linear
/
/ US-08-804-444A-24
/
Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: Gaps: 0
US-10-635-908-15 (1-214) x US-08-804-444A-24 (1-714)
QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGTCTCAAAATTCATGTCATCCATGAGAGACAGGGGTCAAC 129
QY 21 ILeThrCValYeaIAspSerGlnAnValIValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 130 GTACACCTGCAGAGCCAGTCAGATGGGTACTAATGTAGTCCGTGGATCAACAGAAACCA 189
QY 41 GLYGlnSerProLysLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTCTTAACACCTGATTTTCTGTCTACTCTACCGGTACAGTGGATCTCTGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAnMetGlnSer 80
DB 250 CGGTCACAGGAGCGATGCGATCTGGACAGATTTCATCTACCATCAGCATGCGCATGGAGTCT 309
QY 81 GIuAspLeuAlaAspPhePheCysGlnGlnIleTyrSerAsnTyrProTrpThrPheGlyGly 100
DB 310 GAAGACTTGGCAGACTTATTCGTCTGACGACATATATACATCATCTCTCAGCTTCGCTCT 369
QY 101 GIuThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 370 GGGACCAAGCTGAGCTTCGACAGAGCTGGGCTGCGACCATCTCTTCATCTTCCGGCCA 429
QY 121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAnAsnPheTyr 140
DB 430 TCTGATGAGAGAGTTGAATCTGGAACCTGCTTCTGTGTGTGCTGCTGATTAATCTTCTAT 489
```

```

QY 141 ProArgGluAlaLysValGlnTrpLysValAspAnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCCAGAGAGGCGCAAGTGAAGTGAATTAAGCCCTTCATTCGGATTAATCCAG 549
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGACTGTCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 609
QY 181 LeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200
DB 610 CTGAGCAAAAGCAGACTAGAGAAAACAAAGCTTACGCTCGAAGTCACCATCAGAGGC 669
QY 201 LeuSerSerProValThrLysSerPheAnArgGlyGlyCys 214
DB 670 CTGAGCTGCGCGTCAAAAGGCTTCAACAGGGGAGAGTGT 711
/
/ RESULT 8
/ US-09-026-985-24
/ Sequence 24, Application US/09026985
/ Patent No. 6133426
/
/ GENERAL INFORMATION:
/ APPLICANT: Gonzalez, Tania R.
/ APPLICANT: Leong, Steven R.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
/ TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
/ NUMBER OF SEQUENCES: 72
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpatin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/026,985
/ FILING DATE: 20-Feb-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P1085R3-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/952-9881
/ TELEFAX: 650/225-5530
/
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Double
/ TOPOLOGY: Linear
/
/ US-09-026-985-24
/
Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: Gaps: 0
US-10-635-908-15 (1-214) x US-09-026-985-24 (1-714)
QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGTCTCAAAATTCATGTCATCCATGAGAGACAGGGGTCAAC 129
```



21 ILeThrCysLysAlaSerGlnSerValValSerAlaValAlaTrpTyrGlnGlnLysPro 40  
130 GTCACTGCAAGGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189  
41 GlnGlnSerProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60  
190 GGGCAATCTCTTAAACACATGATTTACTGCTCATCTTACCGGTACGAGTGGAGTCCCTGAT 249  
61 ArgPheThrGlnGlnSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
250 CGCTTACAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 309  
81 GluAspLeuAlaAspPhePheCysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
310 GAAGACTTGGCAGACATATTTCTGTCAGCATATATATATATATATATATATATATATAT 369  
101 GlyThrLysLeuGlnLeuLysSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 120  
370 GGGACCAAGCTGAGCTTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429  
121 SerAspGlnGlnLeuLysSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140  
430 TCTGATGAGCAGTGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 489  
141 ProArgGlnAlaLysValGlnTrpLysValAlaAspAsnAlaLeuGlnSerGlnGlnSerGln 160  
490 CCGAGAGAGCCCAAGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 549  
161 GluSerValThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180  
550 GAGAGTCTCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 609  
181 LeuSerLysAlaAspTyrGlnLysValLysValLysValLysValLysValLysValLys 200  
610 CTGAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 669  
201 LeuSerSerProValThrLysSerPheAsnArgLysGlnCys 214  
670 CTGAGCTCGCCCGTCAAGAGAGCTTCAACAGGGGAGAGTGT 711

RESULT 9  
US-09-121-952A-24  
Sequence 24, Application US/09121952A  
Patent No. 6458355  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc., Hsei, Vanessa  
APPLICANT: Koumenis, Iphigenia  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Shahrokh, Zahra  
APPLICANT: Zapata, Gerardo A.  
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONUGATES  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/121,952A  
FILING DATE: 24-Jul-1998  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/074330  
FILING DATE: 22-JAN-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/075467  
FILING DATE: 20-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085R4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 714 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
US-09-121-952A-24  
Alignment Scores:  
Pred. No.: 1,86e-112 Length: 714  
Score: 1017.00 Matches: 194  
Percent Similarity: 96.3% Conservative: 12  
Best Local Similarity: 90.7% Mismatches: 8  
Query Match: 91.1% Indels: 0  
Gaps: 0  
US-10-635-908-15 (1-214) x US-09-121-952A-24 (1-714)  
1 AspIleValMetThrGlnSerGlnArgPheMetSerThrValGlyAspArgValSer 20  
70 GATATGTCATGACACAGTCTCAAAAATTCATCTCCACATCAGTAGAGACAGGAGTACG 129  
21 ILeThrCysLysAlaSerGlnSerValValSerAlaValAlaTrpTyrGlnGlnLysPro 40  
130 GTCACTGCAAGGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189  
41 GlnGlnSerProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60  
190 GGGCAATCTCTTAAACACATGATTTACTGCTCATCTTACCGGTACGAGTGGAGTCCCTGAT 249  
61 ArgPheThrGlnGlnSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
250 CGCTTACAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 309  
81 GluAspLeuAlaAspPhePheCysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
310 GAAGACTTGGCAGACATATTTCTGTCAGCATATATATATATATATATATATATATATAT 369  
101 GlyThrLysLeuGlnLeuLysSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 120  
370 GGGACCAAGCTGAGCTTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429  
121 SerAspGlnGlnLeuLysSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140  
430 TCTGATGAGCAGTGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 489  
141 ProArgGlnAlaLysValGlnTrpLysValAlaAspAsnAlaLeuGlnSerGlnGlnSerGln 160  
490 CCGAGAGAGCCCAAGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 549  
161 GluSerValThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180  
550 GAGAGTCTCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 609  
181 LeuSerLysAlaAspTyrGlnLysValLysValLysValLysValLysValLysValLys 200  
610 CTGAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 669  
201 LeuSerSerProValThrLysSerPheAsnArgLysGlnCys 214  
670 CTGAGCTCGCCCGTCAAGAGAGCTTCAACAGGGGAGAGTGT 711

RESULT 10

US-09-234-340A-24  
Sequence 24, Application US/09234340A  
Patent No. 6468532  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc., Haei, Vanessa  
APPLICANT: Koumenis, Iphigenia  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Shahrokh, Zahra  
APPLICANT: Zapata, Gerardo A.  
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/234,340A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/121,952  
FILING DATE: 24-Jul-1998  
APPLICATION NUMBER: 60/074330  
FILING DATE: 22-Jan-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/075467  
FILING DATE: 20-Feb-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085R4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 714 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
US-09-234-340A-24  
Alignment Scores:  
Pred. No.: 1,866-112 Length: 714  
Score: 1017.00 Matches: 194  
Percent Similarity: 96.3% Conservative: 12  
Best Local Similarity: 90.7% Mismatches: 8  
Query Match: 91.1% Indels: 0  
Gaps: 0  
US-10-635-908-15 (1-214) x US-09-234-340A-24 (1-714)  
QY 1 Aspllevalmethrnginserginaargphnemetserthryvalgllyaspargvalser 20  
DB 70 GATATGTCATGACACAGTCTCAAAAATTCATGTCCACATCAGTAGAGACAGGTCAGC 129  
QY 21 IletthCyelysalaserinaanvalvalaserlavalalatrpyrtynginglnlyspro 40  
DB 130 GTACCTCGCAAGCCAGTCAGATGTGGTACTAATGTAAGCTCGTATCAACAGAAACCA 189  
QY 41 GlylnserProlylsleuleuiletyrSerlaseranargtyrThrglyValProasp 60  
DB 190 GGGCAATCTCTTAAGACACTGATTACTCGTCACTCAACCGGTACAGTGGAGTCCCTGAT 249

QY 61 ArgpnehrnglyserglyserglythraapnehrleuThrleSeranmetginsar 80  
DB 250 CGCTTCACAGGACGATGATCTGGACAGATTTCACCTACCATCAGCATGGCAGTGTCT 309  
QY 81 GluaSplleualAAsPhePheCysglnGlnTySerAsnTyProTrpThrPhegly 100  
DB 310 GAAAGCTTGACAGACTATTCTGTGACGAATATACATCATTCCTCAGTTCCGTCC 369  
QY 101 GlyThrlyLeuGlnllylsahgthrValalalAProSerValPhelePhePro 120  
DB 370 GGGACCAAGCTGGAGCTTGAAGAGCTGTGGTCACCTCTGTCTTCATCTTCCGCCA 429  
QY 121 SeraspGlnGlnleuLyserglythraaserlavalCysleuLeuananpnehyr 140  
DB 430 TCTGATGACAGCTGAAATCTGAACTGCTTGTTGTGTGCTGTGAATATCTTAT 489  
QY 141 ProArgGluAlalyValGlnTrpLyValAAsPasnAlaleuGlnserGlyansergln 160  
DB 490 CCCAGAGAGCCCAAGTACAGTGAAGTGAATACGCCCTCAATCGGGTAATCCCA 549  
QY 161 GluSerValThrGluGlnAAsPserLyAAsPserThrTySerleuSerSerThrleuThr 180  
DB 550 GAGAGTGTCAAGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 609  
QY 181 LeuSerLyAlAAsPTrgGlnlylsahlyVallyrAlaCysGlnValThrHsglnGly 200  
DB 610 CTGAGCAAGACAGACTACGAAACACAAAGTCTACCTCGCAATCACCCTACGGGC 669  
QY 201 LeuSerSerProValThrlySerPheanarglyGlyCys 214  
DB 670 CTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGAGAGTGT 711  
RESULT 11  
US-09-355-014-24  
Sequence 24, Application US/09355014  
Patent No. 6870033  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc., Haei, Vanessa  
APPLICANT: Koumenis, Iphigenia  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Shahrokh, Zahra  
APPLICANT: Zapata, Gerardo A.  
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/355,014  
FILING DATE: 21-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085R3PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 714 base pairs

TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-09-355-014-24

Alignment Scores:  
Pred. No.: 1,866-112 Length: 714  
Score: 1017.00 Matches: 194  
Percent Similarity: 96.3% Conservative: 12  
Best Local Similarity: 90.7% Mismatches: 8  
Query Match: 91.1% Indels: 0  
DB: 3 Gaps: 0

US-10-635-908-15 (1-214) x US-09-355-014-24 (1-714)

```
QY 1 Aspl1eValMetThrgInSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGTCTCAAAATTCATGCTCCACATCAGTAGAGACAGGCTCAGC 129
QY 21 IleThrCysAlaSerGlnAsnValSerAlaValAlaTPrTyrGlnGlnLysPro 40
DB 130 GTACCTCGAAGGCGAGTCAAGATGGGTACTATATAGCTGGTATCAACAGAAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTTAAGACATGATTTACTCGTCATCCGATACCGGTACAGTAGGATCCCGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGGAGTGGATCTGGGACAGATTTCACTCTCCACATCAGCCATGTGTCAGTCT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTPrThrPheGlyGly 100
DB 310 GAAGACTTGGACGCTATTTCTGTGCACAAATATACCTATCTCTCAGCTTCGCTCT 369
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 370 GGGACCAAGCTGAGCTTCAAGAGCTGGCTGCACATCTGCTTCATCTTCCCGCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 430 TCTGATGAGCAGTTGGAATCTGGAACCTCTTCTGTGTGCTCGCTGGAATATCTTCTAT 489
QY 141 ProArgGlnAlaLysValGlnTPrLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCCAGAGAGGCGAAAGTACAGTGAAGGTGATTAACGCCCTCCATGCGGTAACTCCGAG 549
QY 161 GluSerValThrgInGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGAGTCTCAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 609
QY 181 LeuSerLysAlaAspTyrGlyLysIleLysValIleValCysGluValThrHisGlnGly 200
DB 610 CTGAGCAAGCAGACGACTACGAGAAACACAAAGCTTACGCTCCGAAAGTCAACCATCAGG 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB 670 CTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 711
```

## RESULT 12

US-09-726-258-24  
Sequence 24 Application US/09726258

Patent No. 7005504  
GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Hseil, Vanessa  
APPLICANT: Koumenis, Iphigenia

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

APPLICANT: Shabrokh, Zahra

APPLICANT: Zapata, Gerardo A.

TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND  
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES

## NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/726,258

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/234,182

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/094003

FILING DATE: 24-JUL-1998

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085R4-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SBO ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 714 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Double

TOPOLOGY: Linear

US-09-726-258-24

## Alignment Scores:

Pred. No.: 1,866-112 Length: 714  
Score: 1017.00 Matches: 194  
Percent Similarity: 96.3% Conservative: 12  
Best Local Similarity: 90.7% Mismatches: 8  
Query Match: 91.1% Indels: 0  
DB: 5 Gaps: 0

US-10-635-908-15 (1-214) x US-09-726-258-24 (1-714)

```
QY 1 Aspl1eValMetThrgInSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGTCTCAAAATTCATGCTCCACATCAGTAGAGACAGGCTCAGC 129
QY 21 IleThrCysAlaSerGlnAsnValSerAlaValAlaTPrTyrGlnGlnLysPro 40
DB 130 GTACCTCGAAGGCGAGTCAAGATGGGTACTATATAGCTGGTATCAACAGAAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTTAAGACATGATTTACTCGTCATCCGATACCGGTACAGTAGGATCCCGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGGAGTGGATCTGGGACAGATTTCACTCTCCACATCAGCCATGTGTCAGTCT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTPrThrPheGlyGly 100
DB 310 GAAGACTTGGACGCTATTTCTGTGCACAAATATACCTATCTCTCAGCTTCGCTCT 369
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 370 GGGACCAAGCTGAGCTTCAAGAGCTGGCTGCACATCTGCTTCATCTTCCCGCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
```

DB 430 TCTGATGACGACGTGAATCTGAACCTCTTCTGTGTGTGCTGTGATTAATCTTCTAT 489  
QY 141 ProATGGLUALALysValGlnTrpIlyValAAspAsnAlaLeuGlnSerGlyAnsSerGln 160  
DB 490 CCCAAGAGAGCCAAAGTACAGTGAAGGTGAATACGCCCTCCAAATCGGGTAATCTCCAG 549  
QY 161 GluSerValThrGluGlnAspSerIlyAspSerThrTyrSerLeuSerSerThrLeuThr 180  
DB 550 GAGAGTGTACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 609  
QY 181 LeuSerIlyAlaAspTyrGluIlySerIlyValAlaCysGluValThrHisGlnGly 200  
DB 610 CTGAGCAAGACGACACTACAGAAACACAAAGTCTACGCTCGGAATCACCATTACGGCC 669  
QY 201 LeuSerSerProValThrIlySerPheAsnArgGlyGlyCys 214  
DB 670 CTGAGCTGCGCCGTCAACAAAGAGCTTCAACAGGGAGAGTGT 711  
RESULT 13  
US-09-875-221B-127  
Sequence 127, Application US/09875221B  
Patent No. 7012135  
GENERAL INFORMATION:  
APPLICANT: Achwal, Diljeet Singh  
APPLICANT: Brown, Derek Thomas  
APPLICANT: Weir, Andrew Neil Charles  
APPLICANT: Popplewell, Andrew George  
APPLICANT: Chapman, Andrew Paul  
APPLICANT: King, David John  
TITLE OF INVENTION: Biological Products  
FILE REFERENCE: CAP-0089  
CURRENT APPLICATION NUMBER: US/09/875,221B  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: GB0013810.7  
NUMBER OF SEQ ID NOS: 130  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 127  
LENGTH: 642  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Grafted light chain for fab and modified fab  
US-09-875-221B-127  
Alignment Scores:  
Pred. No.: 3,02e-104 Length: 642  
Score: 948.00 Matches: 183  
Percent Similarity: 92.1% Conservative: 14  
Best Local Similarity: 85.5% Mismatches: 17  
Query Match: 84.9% Indels: 0  
Gaps: 0  
US-10-635-908-15 (1-214) x US-09-875-221B-127 (1-642)  
QY 1 AspIleValMetThrGlnSerGlnAspMetSerThrThyValGlyAspArgValSer 20  
DB 1 GACATTCAATGATGCCAGGCCCATCCAGCTCAGCTCTTCTATATGTGTGTACCATAC 60  
QY 21 IleThrCysIlyValAspSerGlnAsnValIleSerAlaValAlaIleTrpIlyGlnIlyPro 40  
DB 61 ATCACTTGTAAACCCGATCGAAGCGTAGAGTACTAAGTACCTGGTATCAGCAAAACCA 120  
QY 41 GlyIleSerProIlyLeuLeuIleIlySerAlaSerAsnArgTyrThrGlyValProAsp 60  
DB 121 GGTAAGACCCCAAAAGCCCTCATCTACAGTGCTCTTCTCTATATGTGTGTACCATAC 180  
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80  
DB 181 AGGTTTACGGGATCCCGTACTGTACTGATTTACCCCTCAGATCAGTACCTCCAGCCA 240  
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIlySerAsnIlyProTrpThrPheGlyGly 100

DB 241 GAAAGTTTCCGCCACTTATTAAGTACAGTAAATTAACATTATCCACTCATTCGGTCAG 300  
QY 101 GlyThrIlyLeuGluIleIlySerArgThrValAlaAlaProSerValPheIlePhePro 120  
DB 301 GGTAATTAAGTGAATCAACGTAAGTACGGGCCCCCATCTGTCTTCACTTCCCGCCA 360  
QY 121 SerAspGluGlnIleLeuIlySerGlyThrAlaSerValIleCysLeuLeuAsnAspPheTyr 140  
DB 361 TCTGATGACGACCTTAATCTGAACCTGCTGTGTGTGCTGTGATTAATCTTCTAT 420  
QY 141 ProATGGLUALALysValGlnTrpIlyValAAspAsnAlaLeuGlnSerGlyAnsSerGln 160  
DB 421 CCCAAGAGAGCCAAAGTACAGTGAAGGTGAATACGCCCTCCAAATCGGGTAATCTCCAG 480  
QY 161 GluSerValThrGluGlnAspSerIlyAspSerThrTyrSerLeuSerSerThrLeuThr 180  
DB 481 GAGAGTGTACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 540  
QY 181 LeuSerIlyAlaAspTyrGluIlySerIlyValAlaCysGluValThrHisGlnGly 200  
DB 541 CTGAGCAAGACGACACTACAGAAACACAAAGTCTACGCTCGGAATCACCATTACGGCC 600  
QY 201 LeuSerSerProValThrIlySerPheAsnArgGlyGlyCys 214  
DB 601 CTGAGCTCACCAGTAAACAAAGCTTATTAAGAGAGAGTGT 642  
RESULT 14  
US-08-030-175-3  
Sequence 3, Application US/08030175  
Patent No. 6757996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Rothwell, Pigg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW, Suite 701 East  
CITY: Washington  
STATE: D. C.  
COUNTRY: U.S.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage  
COMPUTER: IBM AT compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
SOFTWARE: Wordperfect 5.0 (dos Text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,175  
FILING DATE: 17-MAY-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB91/01578  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ernst, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1768-113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 748 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULAR TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO





GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 06:54:05 ; Search time 1471.01 Seconds  
(without alignments)  
2681.378 Million cell updates/sec

Title: US-10-635-908-15

Perfect score: 1116  
Sequence: 1 DIVMTQSGQFMSTVTGDRVS.....EVTHQGLSGPVTKSFNRGEC 214

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-Q=/abs/ABSSWB.spool/US10635908/runat\_02062006\_104222\_10380/app\_query.fasta-1  
-DB=Published Applications NA Main -QMT=faetap -SUFIX=rnphm -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abs02h  
-USER=US10635908.@CGN 1.1.2326.@runat\_02062006\_104222\_10380 -NCPU=6 -ICPU=3  
-N0 MAMP -NEG SCORES=0 -WAIT -DISPATCH=100 -LONGLOG -DEV TIMEOUT=120  
-NARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:

1: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US08\_PUBCOMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US09\_PUBCOMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10\_PUBCOMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
11: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
12: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11\_PUBCOMB.seq:\*  
13: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11B\_PUBCOMB.seq:\*  
14: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11C\_PUBCOMB.seq:\*  
15: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11D\_PUBCOMB.seq:\*  
16: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11E\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	91.1	714	3	US-09-726-258-24 Sequence 24, Appl

2	1017	91.1	714	16	US-11-259-232-24	Sequence 24, Appl
3	977.5	87.6	699	13	US-11-020-508-14	Sequence 14, Appl
4	964	86.4	862	16	US-11-218-813-129	Sequence 129, App
5	964	86.4	12514	9	US-10-714-000-16	Sequence 16, Appl
6	964	86.4	12514	9	US-10-715-270-4	Sequence 4, Appl1
7	956	85.7	702	7	US-10-377-121-15	Sequence 15, Appl1
8	956	85.7	702	7	US-10-377-121-19	Sequence 19, Appl1
9	954.5	85.5	711	7	US-10-281-478A-55	Sequence 55, Appl1
10	954.5	85.5	711	7	US-10-275-180A-55	Sequence 55, Appl1
11	954.5	85.5	711	7	US-10-286-132A-55	Sequence 55, Appl1
12	948	84.9	642	3	US-09-949-559-127	Sequence 127, App
13	948	84.9	642	7	US-09-875-221A-127	Sequence 127, App
14	948	84.9	642	7	US-10-310-454-3	Sequence 3, Appl1
15	945	84.7	708	7	US-10-401-344-3	Sequence 3, Appl1
16	945	84.7	708	7	US-10-986-496-6	Sequence 6, Appl1
17	944	84.6	642	9	US-10-914-015-112	Sequence 112, App
18	943	84.5	660	6	US-09-995-693-3	Sequence 3, Appl1
19	943	84.5	660	6	US-10-232-408-3	Sequence 3, Appl1
20	939.5	84.2	928	7	US-10-221-945-5	Sequence 5, Appl1
21	938	84.1	1710	7	US-10-291-265-99	Sequence 99, Appl1
22	938	84.1	1710	15	US-11-000-463-99	Sequence 99, Appl1
23	936	83.9	705	7	US-10-292-088-23	Sequence 23, Appl1
24	936	83.9	974	3	US-09-859-053-29	Sequence 29, Appl1
25	936	83.9	974	9	US-10-800-250-29	Sequence 29, Appl1
26	936	83.9	974	9	US-10-625-105-29	Sequence 29, Appl1
27	935	83.8	1404	7	US-10-291-265-663	Sequence 663, App
28	935	83.8	1404	15	US-11-000-463-663	Sequence 663, App
29	935	83.8	1711	10	US-10-901-011-5	Sequence 5, Appl1
30	935	83.8	9231	10	US-10-939-309-28	Sequence 28, Appl1
31	934	83.7	642	10	US-10-644-277-63	Sequence 63, Appl1
32	934	83.7	1477	9	US-10-728-420B-116	Sequence 116, App
33	934	83.7	1477	9	US-10-728-420B-117	Sequence 117, App
34	934	83.7	3300	9	US-10-764-428-24	Sequence 24, Appl1
35	933	83.6	711	10	US-10-910-901-11	Sequence 11, Appl1
36	932	83.5	645	8	US-10-408-901-35	Sequence 35, Appl1
37	932	83.5	3819	16	US-11-009-840A-243	Sequence 243, App
38	932	83.5	3819	16	US-11-009-878A-243	Sequence 243, App
39	932	83.5	3819	16	US-11-009-769A-243	Sequence 243, App
40	931	83.4	660	16	US-11-049-536-702	Sequence 702, App
41	931	83.4	660	16	US-11-199-739-702	Sequence 702, App
42	931	83.4	711	16	US-10-911-739-726	Sequence 726, App
43	931	83.4	1951	6	US-10-011-125-1	Sequence 1, Appl1
44	931	83.4	3255	10	US-10-697-995-10	Sequence 10, Appl1
45	931	83.4	3300	6	US-10-020-786-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-09-726-258-24  
Sequence 24, Application US/09726258  
Publication No. US20030021790A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc., Hsei, Vanessa  
APPLICANT: Komnents, Iphigenia  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Shahrokh, Zahra  
APPLICANT: Zapata, Gerardo A.  
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND  
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

```
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/726,258
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/234,182
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/094003
/ FILING DATE: 24-JUL-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P1085R4-1A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-5530
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Double
/ TOPOLOGY: Linear
/
/ US-09-726-258-24
/
Alignment Scores:
Pred. No.: 2,14e-118 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 0
/
US-10-635-908-15 (1-214) x US-09-726-258-24 (1-714)
QY 1 Aapllevalmethrclnserglnargphemetserthrthrvajllyapargvalser 20
DB 70 GATATGTCATGACACAGCTCAAAATTCATGTCCACATCACTAGAGACAGGTCAGC 129
QY 21 Iletthrcylalyalaaserglinsanvalvalseralvalalatrrpyrglnglnlypro 40
DB 130 GTCACCTGCAAGGCCAGTCAAGATGGGACTCAATGTAAGCCGTGATCAACGAAACCA 189
QY 41 Glylnserprolyseuleuiletyrseralaserasnargtyrthrlyvalproasp 60
DB 190 GGGCAATCTCTTAACACACTGATTACTCGTCACTACCGGACAGTGAAGTCCCTGAT 249
QY 61 Argphethrglyserglyserglythraapphetrleuthrllseseransmetglnser 80
DB 250 CGCTTACAGGCGAGTGTGAGACAGATTCTCACTCCACATCAAGCCATGTGAGTCT 309
QY 81 Gluaspleuualaaaphephecysglnlntyrserasntyrprotrprrhphneglygly 100
DB 310 GAAGACTTGCCACACTATTCTGTCTGACCAATTAACATCTATCTCTCAAGTTCGGTCT 369
QY 101 Glythrlvleuglnleuylsargthrvalajalaiproservalpheilephepropro 120
DB 370 GGGACCAAGCTGAGCTTGGAAAGCTGTGGCTGACCACTCTCTTCACTCTCCGCCCA 429
QY 121 Seraspglunglnleuylserserlythralservalcylseuleuansanpheityr 140
DB 430 TCTGATGACAGCTTGAATCTGAACCTGCTTGTGTGTGCTGCTGAAATTAATCTTAT 489
QY 141 Proarglunialalyvalglntrplyvalaspaanlalenglnserglyaanserghln 160
DB 490 CCCAGAGAGCCCAAGTACAGTGAAGGTGATTAAGCCCTCCAAATCGGTAATCTCCAG 549
QY 161 Gluservalthrjglunlapserlyaspsertthryserleuserserthrleuthr 180
DB 550 GAAGAGTGTCAAGAGCGACAGCAAGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 609
QY 181 Leuserlyvalaaspryrglulvghilevaltyralacybglnvalthrhlsglngly 200
```

```
DB 610 CTGAGCCAAAGCAGCTAGAGAAACAAAGTCTAGGCTGAGGTACCAATCAGGAC 669
QY 201 LeuserSerProvalThrlySerPheasnarglyglycys 214
DB 670 CTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGAGAGGTGT 711
/
RESULT 2
US-11-259-232-24
/ Sequence 24, Application US/11259232
/ Publication No. US20060083683A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc., Hael, Vanessa
/ APPLICANT: Koumenda, Iphigenia
/ APPLICANT: Leong, Steven R.
/ APPLICANT: Shantokh, Zahra
/ APPLICANT: Zapata, Gerardo A.
/ TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND USES OF SAME
/ FILE REFERENCE: P1085R6
/ CURRENT APPLICATION NUMBER: US/11/259,232
/ PRIOR FILING DATE: 2005-10-25
/ PRIOR APPLICATION NUMBER: US/09/489,394
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US 60/116,787
/ PRIOR FILING DATE: 1999-01-21
/ NUMBER OF SEQ ID NOS: 72
/ SEQ ID NO 24
/ LENGTH: 714
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: Artificial Sequence
/ LOCATION: 1-714
/ OTHER INFORMATION: recombinant immunoglobulin
/
US-11-259-232-24
/
Alignment Scores:
Pred. No.: 2,14e-118 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 0
/
US-10-635-908-15 (1-214) x US-11-259-232-24 (1-714)
QY 1 Aapllevalmethrclnserglnargphemetserthrthrvajllyapargvalser 20
DB 70 GATATGTCATGACACAGCTCAAAATTCATGTCCACATCACTAGAGACAGGTCAGC 129
QY 21 Iletthrcylalyalaaserglinsanvalvalseralvalalatrrpyrglnglnlypro 40
DB 130 GTCACCTGCAAGGCCAGTCAAGATGGGACTCAATGTAAGCCGTGATCAACGAAACCA 189
QY 41 Glylnserprolyseuleuiletyrseralaserasnargtyrthrlyvalproasp 60
DB 190 GGGCAATCTCTTAACACACTGATTACTCGTCACTACCGGACAGTGAAGTCCCTGAT 249
QY 61 Argphethrglyserglyserglythraapphetrleuthrllseseransmetglnser 80
DB 250 CGCTTACAGGCGAGTGTGAGACAGATTCTCACTCCACATCAAGCCATGTGAGTCT 309
QY 81 Gluaspleuualaaaphephecysglnlntyrserasntyrprotrprrhphneglygly 100
DB 310 GAAGACTTGCCACACTATTCTGTCTGACCAATTAACATCTATCTCTCAAGTTCGGTCT 369
QY 101 Glythrlvleuglnleuylsargthrvalajalaiproservalpheilephepropro 120
DB 370 GGGACCAAGCTGAGCTTGGAAAGCTGTGGCTGACCACTCTCTTCACTCTCCGCCCA 429
QY 121 Seraspglunglnleuylserserlythralservalcylseuleuansanpheityr 140
DB 430 TCTGATGACAGCTTGAATCTGAACCTGCTTGTGTGTGCTGCTGAAATTAATCTTAT 489
```



```
QY 141 ProArgGluAlaIyValGlnTrpIysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCAGAGAGAGCCCAAGATACAGTGGAGAGTGGATTAAGCCCTCCAAATCGGGTAATCCCAAG 549
QY 161 GluSerValThrGluGlnAspSerIysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGAGGTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609
QY 181 LeuSerIyAlaAspTyrGlyIyShIyIyValIyTyrAlaCysGluValThrHisGlnGly 200
DB 610 CTGAGCAAGAGCAAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 669
QY 201 LeuSerSerProValThrIySerSerPheAsnArgGlyGluCys 214
DB 670 CTGAGCTCGCCGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 711

RESULT 3
US-11-020-508-14
; Sequence 14, Application US/11020508
; GENERAL INFORMATION:
; APPLICANT: CHANG, WESLEY
; APPLICANT: EATON, DAN L.
; APPLICANT: BEHNS, ALLEN JR.
; APPLICANT: DE SAUVAGE, FREDERIC J.
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HONGO, JO-ANNE
; APPLICANT: KOEPPEN, HARTMUT
; APPLICANT: POLSON, ANDREW
; APPLICANT: SMITH, VICTORIA
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor or
; FILE REFERENCE: P51091-US
; CURRENT APPLICATION NUMBER: US/11/020,508
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: PCT/US2004/038262
; PRIOR FILING DATE: 2004-11-16
; PRIOR APPLICATION NUMBER: US 10/989,826
; PRIOR FILING DATE: 2004-11-16
; PRIOR APPLICATION NUMBER: US 60/520,842
; PRIOR FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: PCT/US03/36298
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 10/712,892
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/25892
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 10/241,220
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: PCT/US02/28859
; PRIOR FILING DATE: 2002-09-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 14
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-020-508-14

Alignment Scores:
Pred. No.: 2,16e-113 Length: 699
Score: 977.50 Matches: 190
Percent Similarity: 94.4% Conservative: 12
Best Local Similarity: 88.8% Mismatches: 11
Query Match: 87.6% Indels: 1
DB: 13 Gaps: 1

US-10-635-908-15 (1-214) x US-11-020-508-14 (1-699)
```

```
QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 58 GATATCGTATGATACCCAGATCTCATTAATTCATGTCACATCATGAGAGAGAGAGAGAGAG 117
QY 21 ILeuThrCysIyAlaSerGlnAsnValIleSerAlaValAlaITrpyrGlnGlnIyPro 40
DB 118 ATCTCCGCAAGAGCCAGATGAGATGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 177
QY 41 GlyGlnSerProIySerLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 178 GGCATATTCCTTAAGTACTGATTAATTAATTCGCGGATACCGGATACGAGAGAGAGAGAG 234
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 235 CGCTTCACTGAGAGATGATCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 294
QY 81 GluAspLeuAlaAspPheCysGlnGlnIyIySerAsnTyrProITrpyrPheGlyGly 100
DB 295 GAAGACCTGGCAATTTATTTCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 354
QY 101 GlyThrIyLeuGlnIleIySerArgThrValAlaAlaProSerValPheIlePhePro 120
DB 355 GGTACCAAGGTGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
QY 121 SerAspGluGlnLeuIySerGlyThrAlaSerValIyCysLeuLeuAsnAsnPheTyr 140
DB 415 TCTGATGAGAGAGTGAATCTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 474
QY 141 ProArgGluAlaIyValGlnTrpIyValIyAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 475 CCAGAGAGAGCCCAAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534
QY 161 GluSerValThrGluGlnAspSerIyAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 535 GAGAGGTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 594
QY 181 LeuSerIyAlaAspTyrGlyIyShIyIyValIyTyrAlaCysGluValITrHisGlnGly 200
DB 595 CTGAGCAAGAGCAAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 654
QY 201 LeuSerSerProValThrIySerSerPheAsnArgGlyGluCys 214
DB 655 CTGAGCTCGCCGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 696

RESULT 4
US-11-218-813-129
; Sequence 129, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; PRIOR FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 144
; SEQ ID NO 129
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 862
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain variable and constant region of deJ591
; NAME/KEY: CDS
; LOCATION: (151) ... (849)
US-11-218-813-129

Alignment Scores:
```

Pred. No.: 1.51e-111 Length: 862  
Score: 964.00 Matches: 183  
Percent Similarity: 93.5% Conservative: 17  
Best Local Similarity: 85.5% Mismatches: 14  
Query Match: 86.4% Indels: 0  
DB: 16 Gaps: 0

US-10-635-908-15 (1-214) x US-11-218-813-129 (1-862)

```
QY 1 AapIleValMetThrcInSergInArgPhMetSerThrThrValGlyAspArgValSer 20
   |||||
DB 208 GACATCCAGATACACCAAGTCTCCCTCATCTGTCACATCAGTAGAGACAGGGCTCACC 267
   |||||
QY 21 IletHrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrgInGlnIysPro 40
   |||||
DB 268 CTCACCTGTAAGCCAGTCAAGATGGGTACTGCTGTAGACTGCTATCAACAGAAACCA 327
   |||||
QY 41 GlyInSerProIyLeuLeuIleTySerAlaSerAsnArgTyThrcGlyValProAsp 60
   |||||
DB 328 GGAACCTCTCTTAACCTACTGATTTATTGGGCTTCCACTCGGACACTGGAATCCTTA 387
   |||||
QY 61 ArgPheThrcGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
   |||||
DB 388 CGCTTCTCAGGAGTGAATCTGGGACAGACTTCACTCACCATTCTTAGTCTTCAAGCCT 447
   |||||
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTySerAsnTyProTrpThrPheGlyGly 100
   |||||
DB 448 GAAGACTTTGCAATATTATTAAGTGTGAGCAATATTAACGATTCCTTCAAGTGGTCT 507
   |||||
QY 101 GlyThrIyLeuGlnIleIyAsnArgThrValAlaAlaProSerValPheIlePhePro 120
   |||||
DB 508 GGGACCAAGGTGACATCAACCAACTGTGCTGACACATCTTCTTCACTTCCGCCCA 567
   |||||
QY 121 SerAspGlnGlnIleuIySerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTy 140
   |||||
DB 568 TCTGATGAGCAGATTGAATCTGGAACCTGCTCTGTGTGCTGCTGATTAATCTTCTAT 627
   |||||
QY 141 ProArgGlnAlaIyValGlnTrpIyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
   |||||
DB 628 CCCAGAGAGGCCAAAGTACAGTGAAGGTGATTAAGCCCTCCAAATCGGGTAACTCCCA 687
   |||||
QY 161 GluSerValThrcGlnInAspSerIyAspSerThrTySerLeuSerSerThrLeuThr 180
   |||||
DB 688 GAGAGTCTACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 747
   |||||
QY 181 LeuSerIyAlaAspTyrgIyIyShIyIyValIyTyAlaCysGlnValThrcGlnIy 200
   |||||
DB 748 CTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCAACCCATCAGGGC 807
   |||||
QY 201 LeuSerSerProValThrcIySerPheAsnArgGlyGlyCys 214
   |||||
DB 808 CTGAGCTCGCCCTGTCACAAAGAGCTTCAACAGGGGAGAGTGT 849
   |||||
```

## RESULT 5

US-10-714-000-16  
; Sequence 16, Application US/10714000  
; Publication No. US2005005310A1  
; GENERAL INFORMATION:  
; APPLICANT: Chisholm, Vanessa  
; APPLICANT: Crowley, Craig W.  
; APPLICANT: Krumen, Lynne A.  
; APPLICANT: Meng, Yu-Ju G.  
; TITLE OF INVENTION: EXPRESSION VECTORS AND METHODS  
; FILE REFERENCE: P1746R1P1 US  
; CURRENT APPLICATION NUMBER: US/10/714,000  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: US 10/019,586  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/18841  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: US 60/143,360  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 17

; SEQ ID NO 16  
; LENGTH: 12514  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid pSV.IPD.2C 4 circular ds-DNA  
US-10-714-000-16

## Alignment Scores:

Alignment Scores: 7.03e-110 Length: 12514  
Score: 964.00 Matches: 185  
Percent Similarity: 92.5% Conservative: 13  
Best Local Similarity: 86.4% Mismatches: 16  
Query Match: 86.4% Indels: 0  
DB: 9 Gaps: 0

US-10-635-908-15 (1-214) x US-10-714-000-16 (1-12514)

```
QY 1 AapIleValMetThrcInSergInArgPhMetSerThrThrValGlyAspArgValSer 20
   |||||
DB 4211 GATATCCAGATACACCAAGTCCCGAGCTCCCTGCTCCGCTCTGTGGCGATAGCTCACC 4270
   |||||
QY 21 IletHrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrgInGlnIysPro 40
   |||||
DB 4271 ATCACCCTGCAAGCCAGTCAAGATGTGTATTGGTGTGCTGCTGCTATCAACAGAAACCA 4330
   |||||
QY 41 GlyInSerProIyLeuLeuIleTySerAlaSerAsnArgTyThrcGlyValProAsp 60
   |||||
DB 4331 GGAAGACTCCGAAACTACTGATTTACTGGCTTCTTACCGATACCTGAGATCCCTTCT 4390
   |||||
QY 61 ArgPheThrcGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
   |||||
DB 4391 CGCTTCTCGATCCGCTTCTGGAGCGATTTCACTTCAACATCAAGATGCTGACGCCA 4450
   |||||
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTySerAsnTyProTrpThrPheGlyGly 100
   |||||
DB 4451 GAAGACTTCGCAATATTACTGTCAACATATTATTAATTCCTTCAACAGTTCGACAG 4510
   |||||
QY 101 GlyThrIyLeuGlnIleIyAsnArgThrValAlaAlaProSerValPheIlePhePro 120
   |||||
DB 4511 GGTACCAAGGTGAGATCAACCAACTGTGCTGACACATCTGTCTTCACTTCCGCCCA 4570
   |||||
QY 121 SerAspGlnGlnIleuIySerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTy 140
   |||||
DB 4571 TCTGATGAGCAGATTGAATCTGGAATCTCTGTGTGTGCTGCTGATTAATCTTCTAT 4630
   |||||
QY 141 ProArgGlnAlaIyValGlnTrpIyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
   |||||
DB 4631 CCCAGAGAGGCCAAAGTACAGTGAAGGTGATTAAGCCCTCCAAATCGGGTAACTCCCA 4690
   |||||
QY 161 GluSerValThrcGlnInAspSerIyAspSerThrTySerLeuSerSerThrLeuThr 180
   |||||
DB 4691 GAGAGTGTCAACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 4750
   |||||
QY 181 LeuSerIyAlaAspTyrgIyIyShIyIyValIyTyAlaCysGlnValThrcGlnIy 200
   |||||
DB 4751 CTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCAACCCATCAGGGC 4810
   |||||
QY 201 LeuSerSerProValThrcIySerPheAsnArgGlyGlyCys 214
   |||||
DB 4811 CTGAGCTCGCCCTGTCACAAAGAGCTTCAACAGGGGAGAGTGT 4852
   |||||
```

## RESULT 6

US-10-715-270-4  
; Sequence 4, Application US/10715270  
; Publication No. US20050019925A1  
; GENERAL INFORMATION:  
; APPLICANT: Krumen, Lynne A.  
; APPLICANT: Shen, Amy Y.  
; TITLE OF INVENTION: Inton Fusion Construct and Method of Using for  
; TITLE OF INVENTION: Selecting High-Expressing Production Cell Lines  
; FILE REFERENCE: P1937R1US  
; CURRENT APPLICATION NUMBER: US/10/715,270



QY 121 SerAepGIUGInLeuLySeSerGIYThraLaSeValValCySeLeuLeuAaAaAaPheTyr 140  
Db 418 TCTGATGAGCAAGTTGAAATCTGGAACCTGCTCTGTTGTGTGCTGCTGTAATTAATTTAT 477  
QY 141 ProAAGGUAAlaLySeValGInTrrPlySeValAaPaAnaAlaLeuGInSeRGIYSeSerGIn 160  
Db 478 CCCAAGAGAGCCCAAGTACAGTGAAGGTGATTAACGCTTCATTCGGGTAACTCCAG 537  
QY 161 GluSeVal1ThrGIUGInAaPSeSerLyAaPSeSerThrYrSeSerLeuSeSerThrLeuThr 180  
Db 538 GAGAGTGTCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 597  
QY 181 LeuSeLySeValAaPSeSerGIYLySeVal1YrAlaCySeGluVal1ThrHiSeGInGly 200  
Db 598 CTGAGCAAG 657  
QY 201 LeuSeSerProVal1ThrLySeSerPheAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 214  
Db 658 CTGAGCTGCGCCGTCAAG 699

## RESULT 8

US-10-377-121-19  
Sequence 19, Application US/10377121  
Publication No. US20040001825A1  
GENERAL INFORMATION:  
APPLICANT: GOVINDAM, SERENGULAM  
APPLICANT: OU, ZHENGXING  
APPLICANT: HANSEN, HANS  
APPLICANT: GOLDENBERG, DAVID  
TITLE OF INVENTION: RS7 ANTIBODIES  
FILE REFERENCE: 018733/1163  
CURRENT APPLICATION NUMBER: US/10/377,121  
CURRENT FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: 60/360,299  
PRIOR FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19  
LENGTH: 702  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(699)  
US-10-377-121-19

## Alignment Scores:

Pred. No.: 1,17e-110 Length: 702  
Score: 956.00 Matches: 185  
Percent Similarity: 92.5% Conservative: 13  
Best Local Similarity: 86.4% Mismatches: 16  
Query Match: 85.7% Indels: 0  
DB: 7 Gaps: 0

US-10-635-908-15 (1-214) x US-10-377-121-19 (1-702)

QY 1 AepIeValMeThrGInSeSerGInAaPSeSerThrThraValGIYSeAaPSeValSeR 20  
Db 58 GACATCAGCTGACCCAGTCTCATCTCTGTCGATCTGTAGAGAGACAGAGTCCAGC 117  
QY 21 ILeThCyLySeValAaPSeSerGInAaPSeValSeRAlaValAlaTrPlyGInGInLySePro 40  
Db 118 ATCACCCTGCAAGCCAGTCAAGATGTGATATTGCTGATCCCTGATTCAGCAGAAACCA 177  
QY 41 GIUGInSeProLySeLeuLeu1LeYrSeSerAlaSeSerAaAaAaAaAaAaAaAaAaAaAa 60  
Db 178 GGGAAAGCCCTTAAGTCTGATCTACTCGGATCTCAACGGATCACTGAGAGTCCCTGAT 237  
QY 61 AaPSeThrGInLySeSerGIYThraPSeThrLeuThr1LeSeAaAaAaAaAaAaAaAaAa 80  
Db 238 AGGTTCAAGTGTGATCTGAGAGAGAGATTTCACTCAACATCAGACAGTCTGCAACT 297  
QY 81 GIUGInSeAaAaPSePheCySeGInGInLySeSerAaAaAaAaAaAaAaAaAaAaAaAa 100

Db 238 GAAAGATTTTGGCAATTATTACTGACAGCAATTTATTAATTAATTAATTAATTAATTAAT 357  
QY 101 GIYThrLySeLeuGIn1LeYSeArThrValAlaAaProSeValPhe1LePheProPro 120  
Db 358 GGGACCAAGCTGAGATCAAGCTACTGTGCTGACCATCTGTCTTACTTCTCCGCCCA 417  
QY 121 SerAepGIUGInLeuLySeSerGIYThraLaSeValValCySeLeuLeuAaAaAaPheTyr 140  
Db 418 TCTGATGAGCAAGTTGAAATCTGGAACCTGCTCTGTTGTGTGCTGCTGTAATTAATTTAT 477  
QY 141 ProAAGGUAAlaLySeValGInTrrPlySeValAaPaAnaAlaLeuGInSeRGIYSeSerGIn 160  
Db 478 CCCAAGAGAGCCCAAGTACAGTGAAGGTGATTAACGCTTCATTCGGGTAACTCCAG 537  
QY 161 GluSeVal1ThrGIUGInAaPSeSerLyAaPSeSerThrYrSeSerLeuSeSerThrLeuThr 180  
Db 538 GAGAGTGTCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 597  
QY 181 LeuSeLySeValAaPSeSerGIYLySeVal1YrAlaCySeGluVal1ThrHiSeGInGly 200  
Db 598 CTGAGCAAG 657  
QY 201 LeuSeSerProVal1ThrLySeSerPheAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 214  
Db 658 CTGAGCTGCGCCGTCAAG 699

## RESULT 9

US-10-281-479A-55  
Sequence 55, Application US/10281479A  
Publication No. US20030133932A1  
GENERAL INFORMATION:  
APPLICANT: The UAB Research Foundation  
APPLICANT: Zhou, Tong  
APPLICANT: Ichikawa, Kimihisa  
APPLICANT: Kimberly, Robert P.  
APPLICANT: Koopman, William J.  
APPLICANT: Oshumi, Jun  
APPLICANT: Lobuglio, Albert S.  
APPLICANT: Buchsbaum, Donald J.  
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS  
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THE  
TITLE OF INVENTION: AGENTS  
FILE REFERENCE: 21085.002906  
CURRENT APPLICATION NUMBER: US/10/281,479A  
CURRENT FILING DATE: 2003-01-28  
PRIOR APPLICATION NUMBER: 60/391,478  
PRIOR FILING DATE: 2002-06-24  
PRIOR APPLICATION NUMBER: 60/346,402  
PRIOR FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: PCT/US01/14151  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,344  
PRIOR FILING DATE: 2000-05-02  
NUMBER OF SEQ ID NOS: 102  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 55  
LENGTH: 711  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: /No. US20030133932A1e = Synth  
US-10-281-479A-55

## Alignment Scores:

Pred. No.: 1,84e-110 Length: 711  
Score: 954.50 Matches: 185  
Percent Similarity: 93.5% Conservative: 15  
Best Local Similarity: 86.4% Mismatches: 13  
Query Match: 85.5% Indels: 1  
DB: 7 Gaps: 1

US-10-635-908-15 (1-214) x US-10-281-479A-55 (1-711)



```
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO: 55
/ LENGTH: 711
/ TYPE: DNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-55

Alignment Scores:
Pred. No.: 1,84e-110 Length: 711
Score: 954.50 Matches: 165
Percent Similarity: 93.5% Conservative: 15
Best Local Similarity: 86.4% Mismatches: 13
Query Match: 85.5% Indels: 1
DB: Gaps: 7

US-10-635-908-15 (1-214) x US-10-286-132A-55 (1-711)

QY 1 AapllevalmetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
Db 61 GACATTGTATGACCCCAATCTCCAGTCTTGTCTGCACTCTGGGGGACAGGGGTCAACC 120
QY 21 IletHrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnPro 40
Db 121 ATCACTTGCAAGGCGCATGCAAGATGGGTACTGCTGAGCTGTGATCAACAGAAACCA 180
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db 181 GGGAAAGCTCTTAACCTAGATTTACTGGGATTCACCCGGACACTGGGGTCCCAAGC 240
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 241 AGGTTAGGCGAGCGTGGTCTGGACAGACTTCACCTCACTCTGTGTCGACGCCG 300
QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
Db 301 GAGGATTTTGCACCTATTACTGTCAAGCAATATAGTATATCGG--ACGTTCCGATCA 357
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 358 GGCACCAAGGTGAAATCAACCGCATGTGGTGCAACATCTGTCTTCACTTCCGCCCA 417
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
Db 418 TCTGATGAGCAGTTGAATCTGGAACCTGCTGTGTGTGCTGTGATTAATCTTCTAT 477
QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 478 CCCAGAGAGGCCAAAGTACGTGAAAGTGGATTAAGCCCTCCAAATCGGGTAATCTCCAG 537
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db 538 GAGAGTGTCAACAGCAGCAGCAGCAAGACAGCAGCAGCCTCAGCAGCAGCCTCGAGC 597
QY 181 LeuSerLysAlaAspTyrGlnLysValLysValTyrAlaCysGlnValThrIleGlnGly 200
Db 598 CTGAGCAAAAGCACTACGAGAAACCAAAAGTCTAGCCCTGCGAAAGTCAACCATCAGGGC 657
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlnCys 214
Db 658 CTGAGCTCGCCCTCACAAAGAGCTTCAACAGGGGAGAGTGT 699

RESULT 12
US-09-949-559-127
/ Sequence 127, Application US/09949559
/ Patent No. US20020151682A1
/ GENERAL INFORMATION:
/ APPLICANT: Attnwal, Diljeet Singh
/ APPLICANT: Brown, Derek Thomas
/ APPLICANT: Weir, Andrew Neil Charles
/ APPLICANT: Popplewell, Andrew George
```

```
/ APPLICANT: Chapman, Andrew Paul
/ APPLICANT: King, David John
/ TITLE OF INVENTION: Biological Products
/ FILE REFERENCE: Carp-0095
/ CURRENT APPLICATION NUMBER: US/09/949,559
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 0013810.7GB
/ PRIOR FILING DATE: 2000-06-06
/ PRIOR APPLICATION NUMBER: 09/875,221
/ NUMBER OF SEQ ID NOS: 130
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO: 127
/ LENGTH: 642
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Grafted light chain for fab and modified fab
US-09-949-559-127

Alignment Scores:
Pred. No.: 1,06e-109 Length: 642
Score: 948.00 Matches: 183
Percent Similarity: 92.1% Conservative: 14
Best Local Similarity: 85.5% Mismatches: 17
Query Match: 84.9% Indels: 0
DB: Gaps: 3

US-10-635-908-15 (1-214) x US-09-949-559-127 (1-642)

QY 1 AapllevalmetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
Db 1 GACATTCAATATACCCAGAGCCCATCCAGCCCTGAGGCGATCTGTAGAGACCGGGTCAACC 60
QY 21 IletHrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnPro 40
Db 61 ATCACTTGAAAGCCAGTACAGAACGATGATTAAGTACGTAGCTGTGATACGAAAAACCA 120
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db 121 GGTAAAGCCCAAGCCCTCATCTACAGTGCCTCTTCTCTATAGTGTGTACCATTC 180
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 181 AGGTTACGGGATCCGATGATGATCTTACACCTCAACATCAGTACGATCCCGCCAGCA 240
QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
Db 241 GAAAGATTTGCGCACTATTACTGTCAACAGTATTAACATCTACCCACTCATTCCGCTCAG 300
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 301 GGTACTAAAGGTGAAATCAACGTACGTAGGCGCCCATCTGTCTTCACTTCCGCCCA 360
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
Db 361 TCTGATGAGCAGTTGAATCTGGAATGCTCTGTGTGTGCTGTGATTAATCTTCTAT 420
QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 421 CCCAGAGAGGCCAAAGTACGTGAAAGTGGATTAAGCCCTCCAAATCGGGTAATCTCCAG 480
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db 481 GAGAGTGTCAACAGCAGCAGCAGCAAGACAGCAGCAGCCTCAGCAGCAGCCTCGAGC 540
QY 181 LeuSerLysAlaAspTyrGlnLysValLysValTyrAlaCysGlnValThrIleGlnGly 200
Db 541 CTGAGCAAAAGCACTACGAGAAACCAAAAGTCTAGCCCTGCGAAAGTCAACCATCAGGGC 600
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlnCys 214
Db 601 CTGAGCTCACCAAGTAAACAAAGCTTAAATAGAGAGAGTGT 642
```

## RESULT 13

US-09-875-221A-127  
Sequence 127, Application US/09875221A  
Publication No. US2003026805A1  
GENERAL INFORMATION:  
APPLICANT: Achwal, Diljeet Singh  
APPLICANT: Brown, Derek Thomas  
APPLICANT: Weir, Andrew Neil Charles  
APPLICANT: Popplewell, Andrew George  
APPLICANT: Chapman, Andrew Paul  
APPLICANT: King, David John  
TITLE OF INVENTION: Biological Products  
FILE REFERENCE: Carp-0089  
CURRENT APPLICATION NUMBER: US/09/875,221A  
CURRENT FILING DATE: 2001-06-06  
PRIORITY FILING DATE: 2000-06-06  
PRIORITY FILING DATE: 2000-06-06  
NUMBER OF SEQ ID NOS: 130  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 127  
LENGTH: 642  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Grafted light chain for fab and modified fab  
US-09-875-221A-127

## Alignment Scores:

Pred. No.:	1,06e-109	Length:	642
Score:	948.00	Matches:	183
Percent Similarity:	92.1%	Conservative:	14
Best Local Similarity:	85.5%	Mismatches:	17
Query Match:	84.9%	Indels:	0
DB:	3	Gaps:	0

US-10-635-908-15 (1-214) x US-09-875-221A-127 (1-642)

```
QY 1 Aspl[e]ValMetThrgInserGlnArgPheMetSerThrValGlyAspArgValSer 20
DB 1 GACATTGAATGAGCCAGAGCCCATCCAGCTGAGCGCATGTGAGAGACCGGGTACCC 60
QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 61 ATCCTTGTAAAGCCAGTCAAGAGTACGTACTTAACGTAAGCTGTATCGACAAAACCA 120
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 121 GGTAAAGCCCAAAAGCCCTCATCTACAGTCCCTCTTCTCTATGAGGTGTACCATAC 180
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 181 AGGTTACGCGGATCCGGTAGTGTGATGATTTCAACCTCAGATCAGTAGCCACAGCCA 240
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrThrPheGlyGly 100
DB 241 GAAGTTTCCGCACTTATCTACTGTCAAGATTAACATCACTCCACATTCGGTCCAG 300
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 301 GGTCTAAAGTAAATCAATCAACGTAACGCTACCGGCCCATCTGCTTCATCTCCGCGCA 360
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 361 TCTGATGAGCGAGTGAATCTGAACCTCCTCTGTGTGTGCTGCTCAATTAACCTTCAT 420
QY 141 ProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 421 CCCAGAGAGGCCAAAGTACAGTGAAGGTGATACCGCTCCCATCGGGTAACTCCAG 480
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 481 GAGAGTGTACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 540
```

## RESULT 14

US-10-310-454-3  
Sequence 3, Application US/10310454  
Publication No. US20030157061A1  
GENERAL INFORMATION:  
APPLICANT: Pharmacia Corporation  
TITLE OF INVENTION: Combinations of a Cyclooxygenase-2 Selective Inhibitor and a TNF  
TITLE OF INVENTION: Antagonist and Therapeutic Uses Therefor  
FILE REFERENCE: 18438/09008  
CURRENT APPLICATION NUMBER: US/10/310,454  
CURRENT FILING DATE: 2002-12-05  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 642  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Grafted Light Chain for Fab and Modified Fab  
US-10-310-454-3

## Alignment Scores:

Pred. No.:	1,06e-109	Length:	642
Score:	948.00	Matches:	183
Percent Similarity:	92.1%	Conservative:	14
Best Local Similarity:	85.5%	Mismatches:	17
Query Match:	84.9%	Indels:	0
DB:	7	Gaps:	0

US-10-635-908-15 (1-214) x US-10-310-454-3 (1-642)

```
QY 1 Aspl[e]ValMetThrgInserGlnArgPheMetSerThrValGlyAspArgValSer 20
DB 1 GACATTGAATGAGCCAGAGCCCATCCAGCTGAGCGCATGTGAGAGACCGGGTACCC 60
QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 61 ATCCTTGTAAAGCCAGTCAAGAGTACGTACTTAACGTAAGCTGTATCGACAAAACCA 120
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 121 GGTAAAGCCCAAAAGCCCTCATCTTACAGTCCCTCTTCTCTATGAGGTGTACCATAC 180
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 181 AGGTTACGCGGATCCGGTAGTGTGATGATTTCAACCTCAGATCAGTAGCCACAGCCA 240
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrThrPheGlyGly 100
DB 241 GAAGTTTCCGCACTTATCTACTGTCAAGATTAACATCACTCCACATTCGGTCCAG 300
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 301 GGTCTAAAGTAAATCAATCAACGTAACGCTACCGGCCCATCTGCTTCATCTCCGCGCA 360
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 361 TCTGATGAGCGAGTGAATCTGAACCTCCTGTGTGTGCTGCTCAATTAACCTTCAT 420
QY 141 ProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
```

DB 421 CCCAGAGAGCCCAAGTACAGTGGAGAGTGGATACGCCCTCCATCGGCTACTCCAG 480  
QY 161 GUSerValThrGluGlnAspSerIlyAspSerThrTySerIeuSerSerThrIeuThr 180  
DB 481 GAGAGTGTACAGAGCAGAGCAGACAGACAGACCTACAGCTCAGCAGACCTGACG 540  
QY 181 LeuSerIlyAlaAspTyGluIlyshIlyValIlyValIlyValIlyValIlyValIly 200  
DB 541 CTGAGCAAGCAGACTACAGAAACAAAGCTTACGCTGCGAGTCAACCATCAGGAG 600  
QY 201 LeuSerSerProValThrIlySerPheAsnArgGlyGlyCys 214  
DB 601 CTGAGCTCACCACTAACAAAGCTTAAAGAGAGAGTGT 642

RESULT 15  
US-10-401-344-3  
Sequence 3, Application US/10401344  
Publication No. US20030194404A1  
GENERAL INFORMATION:  
APPLICANT: Schering Corporation and Abgenix, Inc.  
APPLICANT: Greenfeder, Scott  
APPLICANT: Corvalan, Jose  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COMPOSITIONS  
FILE REFERENCE: LI01564MI  
CURRENT APPLICATION NUMBER: US/10/401,344  
CURRENT FILING DATE: 2003-03-27  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 708  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-401-344-3

Alignment Scores:  
pred. No.: 2,94e-109 Length: 708  
Score: 945.00 Matches: 178  
Percent Similarity: 92.5% Conservative: 20  
Best local Similarity: 83.2% Mismatches: 16  
Query Match: 84.7% Indels: 0  
DB: 7 Gaps: 0

US-10-635-908-15 (1-214) X US-10-401-344-3 (1-708)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThyAlaGlyAspArgValSer 20  
DB 67 GACATCGAATGATGACCCAGTCTCCATCCTCCGTGTGTCATCTGTGGAGACAGAGTCACC 126  
QY 21 IleThrCylValAlaSerGlnAsnValValSerAlaValAlaTrpTyGlnGlnIlyPro 40  
DB 127 ATCACTGCGCAGCGAGTCAAGACATTATCACTATTAAATGTATCAGCAGAAACCA 186  
QY 41 GlyGlnSerProIlyLeuIleuIlyTySerAlaSerAsnArgTyThrGlyValProAsp 60  
DB 187 GGGAAAGCCCTTAACTCCTGATCTACAGTGTCTTCCATTGGAAACAGAGTCCATCA 246  
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrIleuThrIleSerAsnMetGlnSer 80  
DB 247 AGGTTCAAGTGAAGTGGTCTGCGAAGATTTTACTTTCACCATCAGCAGAGCTGAGCT 306  
QY 81 GluAspLeuAlaAspPhePheCylGlnGlnIlyTySerAsnTyProTrpThrPheGlyGly 100  
DB 307 GAAGATATTGCAACATATTGTCAACAGTATGATATATCACCGCTCACCTTCGGGCGA 366  
QY 101 GlyThrIlyLeuGlnIlyIlyValArgThrValAlaAlaProSerValPheIlePheProPro 120  
DB 367 GGGACCAAGGTGAGATCAACAGACTGTGCTGCACCATCTGTCTTCACTTCCGCCCA 426  
QY 121 SerAspGlnIleuIlySerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTy 140  
DB 427 TCTGATGAGCAGTGAATCTGGAATGCTGCTGTGTGTGTGCTGGAATTAACCTTCTAT 486

QY 141 ProArgGluAlaIlyValGlnTrpIlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
DB 487 CCCAGAGAGCCCAAGTACAGTGAAGGTGGATTAAGCCCTCCATCGGCTACTCCAG 546  
QY 161 GUSerValThrGluGlnAspSerIlyAspSerThrTySerIeuSerSerThrIeuThr 180  
DB 547 GAGAGTGTACAGAGCAGAGCAGACAGACAGACCTACAGCTCAGCAGACCTGACG 606  
QY 181 LeuSerIlyAlaAspTyGluIlyshIlyValIlyValIlyValIlyValIlyValIly 200  
DB 607 CTGAGCAAGCAGACTACAGAAACAAAGCTTACGCTGCGAAGTCAACCATCAGGAG 666  
QY 201 LeuSerSerProValThrIlySerPheAsnArgGlyGlyCys 214  
DB 667 CTGAGCTCACCACTAACAAAGCTTCAAGAGAGAGTGT 708

Search completed: June 3, 2006, 07:32:32  
Job time: 1481.01 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 3, 2006, 06:56:49 ; Search time 24.4204 Seconds  
(without alignments)  
1548.108 Million cell updates/sec

Title: US-10-635-908-15  
Perfect score: 1116  
Sequence: 1 DVTMTQSQRFMTTVDVRS.....EVTGGLSSPVTKSFNRGHC 214

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Delop 6.0 , Delext 7.0

Searched: 246837 seqs, 5886590 residues  
Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ .p2n.model -DEV=xlh  
-Q=abs/ABSSWB.epool/US10635908/runat.02062006.104226.10433/app.query.fasta.1  
-DB=Published.Applications.NA.New-QEWT=fastap-SUFFIX=trpbn-MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits-START=1-END=1-MATRIX=blomsun62  
-TRANS=human40.cdi-LIST=45-DOCCALIGN=200-THR SCORE=pct-THR MAX=100  
-THR MIN=0 -ALIGN=15-MODE=LOCAL-OUTFMT=ptc-NORM=ext-HEAPSIZE=500-MINLEN=0  
-MAXLEN=2000000000-HOST=abs605h  
-USR=US10635908-@CGN\_1\_1\_26-@runat.02062006.104226.10433-NCPU=6-ICPU=3  
-NO\_MMAP-NEG\_SCORES=0-WAIT-DSPBLOCK=100-LOGNLOG-DEV-TIMEOUT=120  
-MAIN TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FCGAPOP=6-FCGAPEXT=7  
-YGAPOP=10-YGAPEXT=0.5-DELOP=6-DELEXT=7

Database: Published Applications NA.New:\*

1: /BMC\_Celerra\_SIDS3/prodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
2: /BMC\_Celerra\_SIDS3/prodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /BMC\_Celerra\_SIDS3/prodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /BMC\_Celerra\_SIDS3/prodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
5: /BMC\_Celerra\_SIDS3/prodata/2/pubpna/PC1\_NEW\_PUB.seq:\*  
6: /BMC\_Celerra\_SIDS3/prodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
7: /BMC\_Celerra\_SIDS3/prodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
8: /BMC\_Celerra\_SIDS3/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1007	90.2	1701	7	US-11-106-762-10 Sequence 10, Appl
2	964	86.4	862	7	US-11-219-563-129 Sequence 129, Appl
3	937	84.0	642	6	US-10-981-300-17 Sequence 17, Appl
4	936	83.9	705	7	US-11-211-917-23 Sequence 23, Appl
5	934	83.7	705	6	US-10-546-594-131 Sequence 131, Appl
6	933	83.6	642	6	US-10-981-300-13 Sequence 13, Appl
7	929	83.2	645	7	US-11-155-444-3 Sequence 3, Appl
8	928	83.2	705	7	US-11-211-917-47 Sequence 47, Appl
9	901	80.7	705	7	US-11-211-917-87 Sequence 87, Appl

10	900	80.6	645	7	US-11-155-444-19 Sequence 19, Appl
11	878	78.7	705	7	US-11-211-917-71 Sequence 71, Appl
12	872.5	78.2	720	7	US-11-211-917-39 Sequence 39, Appl
13	869.5	77.9	720	7	US-11-211-917-31 Sequence 31, Appl
14	868	77.8	929	7	US-11-293-697-1838 Sequence 1838, Ap
15	867.5	77.7	720	7	US-11-211-917-15 Sequence 15, Appl
16	867.5	77.7	720	7	US-11-211-917-101 Sequence 101, Appl
17	867.5	77.7	9209	7	US-11-183-218-58 Sequence 58, Appl
18	865.5	77.6	720	7	US-11-211-917-7 Sequence 7, Appl
19	865.5	77.6	720	7	US-11-211-917-7 Sequence 55, Appl
20	865.5	77.6	944	7	US-11-293-697-1585 Sequence 1585, Ap
21	864.5	77.5	720	7	US-11-211-917-79 Sequence 79, Appl
22	863.5	77.4	720	7	US-11-211-917-63 Sequence 63, Appl
23	843	75.5	9780	7	US-11-187-863-1 Sequence 1, Appl
24	808.5	72.4	9400	7	US-11-297-317-17 Sequence 17, Appl
25	785.5	70.4	9362	7	US-11-297-317-18 Sequence 18, Appl
26	689.5	61.8	654	6	US-10-506-063A-11 Sequence 11, Appl
27	644.5	57.8	626	6	US-10-506-063A-19 Sequence 19, Appl
28	639	57.3	1810	7	US-11-293-697-1650 Sequence 1650, Ap
29	625	56.0	494	1	US-09-784-950-80 Sequence 80, Appl
30	624	55.9	514	6	US-10-981-300-9 Sequence 9, Appl
31	612	54.8	465	6	US-10-981-300-1 Sequence 1, Appl
32	599	53.7	463	6	US-10-981-300-5 Sequence 5, Appl
33	584.5	52.1	8540	7	US-11-183-218-57 Sequence 57, Appl
34	559	50.4	441	1	US-09-784-950-73 Sequence 73, Appl
35	556	49.8	441	1	US-09-784-950-69 Sequence 69, Appl
36	553	49.6	334	7	US-11-219-563-133 Sequence 133, Appl
37	531	47.6	441	1	US-09-784-950-65 Sequence 65, Appl
38	528	47.3	447	1	US-09-784-950-67 Sequence 67, Appl
39	502.5	45.0	445	1	US-09-784-950-75 Sequence 75, Appl
40	492.5	44.1	431	1	US-09-784-950-71 Sequence 71, Appl
41	484.5	43.4	444	1	US-09-784-950-63 Sequence 63, Appl
42	482.5	43.2	2196	7	US-11-155-444-5 Sequence 5, Appl
43	482.5	43.2	2208	7	US-11-155-444-9 Sequence 9, Appl
44	472	42.3	756	7	US-11-330-353-17 Sequence 17, Appl
45	466	41.8	375	6	US-10-546-594-120 Sequence 120, Appl

## ALIGNMENTS

RESULT 1  
US-11-106-762-10  
; Sequence 10, Application US/11106762  
; Publication No. US20060099662A1  
; GENERAL INFORMATION:  
; APPLICANT: CHUNTHARAPAI, ANAN ET AL.  
; TITLE OF INVENTION: ASSAY FOR ANTIBODIES  
; FILE REFERENCE: P2075R1  
; CURRENT APPLICATION NUMBER: US/11/106,762  
; PRIOR FILING DATE: 2005-04-15  
; PRIORITY APPLICATION NUMBER: US 60/563,193  
; PRIOR FILING DATE: 2004-04-16  
; NUMBER OF SEQ ID NOS: 39  
; SEQ ID NO 10  
; LENGTH: 1701  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: 1684  
; OTHER INFORMATION: Unknown amino acid  
US-11-106-762-10

## Alignment Scores:

Pred. No.: 8.66e-94  
Score: 1007.00  
Percent Similarity: 95.3%  
Best Local Similarity: 90.2%  
Query Match: 90.2%  
DB: 7  
US-10-635-908-15 (1-214) x US-11-106-762-10 (1-1701)

Length: 1701  
Matches: 193  
Conservative: 11  
Mismatch: 10  
Indels: 0  
Gaps: 0

```
QY 1 AspllevalmetThGlnserGlnargPheMetSerThrValGlyAsparGlySer 20
DB 109 GATATCGTATGATGACCAAGTCATGATCCATGATGAGAACAGGGCTCAC 168
QY 21 IletHrCysAlaSerGlnAnanValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 169 GTCACTCGAAGCCGATGATCTGATGATCTGATGATCTGATGATCTGATGAT 228
QY 41 GlnGlnSerProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 229 GGGCAATCTCTTAAACACATGATTTACTGCGCATCTTACCGGATGATGATGAT 288
QY 61 ArgPheThrGlySerGlySerGlyThrArgPheThrLeuThrIleSerAnMetGlnSer 80
DB 289 CGCTTCACAGGCGATGATCTGACAGATTTCACTCAACATCAACATGATGATGAT 348
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGly 100
DB 349 GAAAGACTTGACAGATATTTCTGTCAGCAATATCACAGTTTCCGATGATGAT 408
QY 101 GlyThrLysLeuGlnLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
DB 409 GGATCCAAAGGTGATGATCAACAGATGATGATGATGATGATGATGATGATGAT 468
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValCysLeuLeuAnanPheTyr 140
DB 469 TCTGATGAGCAGTTGAAATCTGAACTGCTTCTGTTGTTGCTGCTGAAATCTTAT 528
QY 141 ProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAnSerGln 160
DB 529 CCCAGAGAGCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 588
QY 161 GluSerValThrGlnLysAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 589 GAGAGTGTCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 648
QY 181 LeuSerLysAlaAspTyrGlyLysLysLysValTyrAlaCysGlnLysValThrIleGlnGly 200
DB 649 CTGAGCAAGCAGACCTACGAGAAACAAAGTCTACGCTGCGAAGTCAACCATCAGGGC 708
QY 201 LeuSerSerProValThrLysSerPheAnanGlyGlyLys 214
DB 709 CTGAGCTCGCCGCTCAACAAAGACTTCAACAGGGGAGAGTGT 750

RESULT 2
US-11-219-563-129
; Sequence 129, Application US/11219563
; Publication No. US2006088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 862
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain variable and constant region of deJ591
; NAME/KEY: CDS
; LOCATION: (151) ... (849)
; US-11-219-563-129
```

```
Alignment Scores:
Score: 8,82e-90
Percent Similarity: 93.5%
Best Local Similarity: 85.5%
Query Match: 86.4%
DB: 7
Gaps: 0

US-10-635-908-15 (1-214) x US-11-219-563-129 (1-862)
QY 1 AspllevalmetThGlnserGlnargPheMetSerThrValGlyAsparGlySer 20
DB 208 GATATCGTATGATGACCAAGTCATGATCCATGATGAGAACAGGGCTCAC 267
QY 21 IletHrCysAlaSerGlnAnanValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 268 CTCACCTGAAAGCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 327
QY 41 GlnGlnSerProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 328 GGAACATCTCTTAAACATGATTTATGAGCATTCATCGGACACTGGAATCTTAA 387
QY 61 ArgPheThrGlySerGlySerGlyThrArgPheThrLeuThrIleSerAnMetGlnSer 80
DB 388 CGCTTCACAGGCGATGATCTGACAGATTTCACTCAACATTCATGATGATGAT 447
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGly 100
DB 448 GAAAGACTTGACAGATATTTACTGATGATGATGATGATGATGATGATGATGAT 507
QY 101 GlyThrLysLeuGlnLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
DB 508 GGGACCAAGTGTGATCAACAGATGATGATGATGATGATGATGATGATGATGAT 567
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValCysLeuLeuAnanPheTyr 140
DB 568 TCTGATGAGCAGTTGAAATCTGAACTGCTTCTGTTGTTGCTGCTGAAATCTTAT 627
QY 141 ProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAnSerGln 160
DB 628 CCAGAGAGAGCCAAAGTATGATGATGATGATGATGATGATGATGATGATGAT 687
QY 161 GluSerValThrGlnLysAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 688 GAGAGTGTCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 747
QY 181 LeuSerLysAlaAspTyrGlyLysLysLysValTyrAlaCysGlnLysValThrIleGlnGly 200
DB 748 CTGAGCAAGCAGACCTACGAGAAACAAAGTCTACGCTGCGAAGTCAACCATCAGGGC 807
QY 201 LeuSerSerProValThrLysSerPheAnanGlyGlyLys 214
DB 808 CTGAGCTCGCCGCTCAACAAAGACTTCAACAGGGGAGAGTGT 849

RESULT 3
US-10-981-300-17
; Sequence 17, Application US/10981300
; Publication No. US2006093599A1
; GENERAL INFORMATION:
; APPLICANT: GADRI GAZIT-BORSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 642
; TYPE: DNA
; ORGANISM: homo sapien
```

US-10-981-300-17

## Alignment Scores:

Pred. No.:	3,41e-87	Length:	642
Score:	937.00	Matches:	177
Percent Similarity:	91.6%	Conservative:	19
Best Local Similarity:	82.7%	Mismatches:	18
Query Match:	84.0%	Indels:	0
DB:	6	Gaps:	0

US-10-635-908-15 (1-214) x US-10-981-300-17 (1-642)

```
QY 1 Aspllevalmethtglnserglnargphmetserththrvallglspargvalser 20
    |||||
    1 GACATCCAGATGACCCAGTCTCCATCCCTCTGTCGATCTGTAGAGACAGAGTCACC 60
    |||||
QY 21 Ilethtcylsyalaserglnasenvalvalseralavalatprrynglnlypro 40
    |||||
    61 ATCATTGCGCGGCGAGTCCAGGCAATTCAGCAATTAATTACCTGTATCAGCAAGAACCA 120
    |||||
QY 41 GLYGLNserProlyseuleuiletyrseralaserasnargtyrthrglyvalproasp 60
    |||||
    121 GGGAAAGTTCTTAAGCTCCGATCTATGCTGATCCCACTTGCAATCAGGGGTCCTCT 180
    |||||
QY 61 Argphethrglyserglyserglythrasphethrleuthrilleserasmecginser 80
    |||||
    181 CGGTTACGTGCGAGTGGATCTGGACAGATTTCACCTCCACATCAGCAGCAGCCCT 240
    |||||
QY 81 Gluaspleualasphethephecysglnintyrsersantyrprotrpnrphneglygly 100
    |||||
    241 GAAGATTTGCAACTTATCTGTCTGCAAAAGTATGACAGTCCCGGTGAGCGTTCGGCA 300
    |||||
QY 101 Glythrlsleuengluileysargthrvallalaproservalpheilepnepro 120
    |||||
    301 GGGACCAAGGTGAAATCAACGACGTGGCTGACCATCTGCTTCACTTCCGCCCA 360
    |||||
QY 121 Seraspoglunleulysserglythralservalvalcysleuleuasnaphetyr 140
    |||||
    361 TCTGATGACGAGTTGAATCTGGAACCTGCTGTGTGCGCTGGAATTAACCTTAT 420
    |||||
QY 141 Proarglualalysvalglntrpvalasphasnaleuenglnserglyasnsergln 160
    |||||
    421 CCCAGAGAGGCCAAAGTACAGTGGAGGTGATTAACCTCCCAATGGGGTAACTCCAG 480
    |||||
QY 161 Gluservalthrngluinaapserlyaspsertthrtyserserleuserserthrlenth 180
    |||||
    481 GAGAGTGTCAACAGCAGGACGACAGCAAGACGACCTACAGCCTCAGAGCAGCCTAGC 540
    |||||
QY 181 Leuserlysalaspyrtyrgluylshlyvaltyralacysgluvalthrhisglngly 200
    |||||
    541 CTGAGCAAGACGACCTACGAGAAACCAAAAGTCTACCGCTCGGAAGTCAACCAACAGGCG 600
    |||||
QY 201 Leuserseprovalthrlyserpheasnargglylucys 214
    |||||
    601 CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGT 642
    |||||
DB 601 CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGT 642
    |||||
RESULT 4
US-11-211-917-23
; Sequence 23, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PP/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
```

PRIOR FILING DATE: 2001-11-09

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: Patencin Ver. 2.1

; SEQ ID NO 23

; LENGTH: 705

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-211-917-23

## Alignment Scores:

Pred. No.:	4,84e-87	Length:	705
Score:	936.00	Matches:	179
Percent Similarity:	91.6%	Conservative:	17
Best Local Similarity:	83.6%	Mismatches:	18
Query Match:	83.9%	Indels:	0
DB:	7	Gaps:	0

US-10-635-908-15 (1-214) x US-11-211-917-23 (1-705)

```
QY 1 Aspllevalmethtglnserglnargphmetserththrvallglspargvalser 20
    |||||
    61 GACATCCAGATGACCCAGTCTCCATCCCTCTGTCGATCTGTAGAGACAGAGTCACC 120
    |||||
QY 21 Ilethtcylsyalaserglnasenvalvalseralavalatprrynglnlypro 40
    |||||
    121 ATCATTGCGCGGCGAGTCCAGGCAATTCAGCAATTAATTACCTGTATCAGCAAGAACCA 180
    |||||
QY 41 GLYGLNserProlyseuleuiletyrseralaserasnargtyrthrglyvalproasp 60
    |||||
    181 GGGAAAGTTCTTAAGCTCCGATCTATGCTGATCCCACTTGCAATCAGGGGTCCTCT 240
    |||||
QY 61 Argphethrglyserglyserglythrasphethrleuthrilleserasmecginser 80
    |||||
    241 AGGTTACGCGCGAGTGGATCTGGACAGATTTCACCTCCACATCAGCAGCAGCCCT 300
    |||||
QY 81 Gluaspleualasphethephecysglnintyrsersantyrprotrpnrphneglygly 100
    |||||
    301 GAAGATTTGCAACTTATCTGTCTGCAAAAGTATGACAGTCCCGGTGAGCGTTCGGCA 360
    |||||
QY 101 Glythrlsleuengluileysargthrvallalaproservalpheilepnepro 120
    |||||
    361 GGGACCAAGGTGAGATCAACGACGTGGCTGACCATCTGCTTCACTTCCGCCCA 420
    |||||
QY 121 Seraspoglunleulysserglythralservalvalcysleuleuasnaphetyr 140
    |||||
    421 TCTGATGACGAGTTGAATCTGGAACCTGCTGTGTGCGCTGGAATTAACCTTAT 480
    |||||
QY 141 Proarglualalysvalglntrpvalasphasnaleuenglnserglyasnsergln 160
    |||||
    481 CCCAGAGAGGCCAAAGTACAGTGGAGGTGATTAACCTCCCAATGGGGTAACTCCAG 540
    |||||
QY 161 Gluservalthrngluinaapserlyaspsertthrtyserserleuserserthrlenth 180
    |||||
    541 GAGAGTGTCAACAGCAGGACGACAGCAAGACGACCTACAGCCTCAGAGCAGCCTAGC 600
    |||||
QY 181 Leuserlysalaspyrtyrgluylshlyvaltyralacysgluvalthrhisglngly 200
    |||||
    601 CTGAGCAAGACGACCTACGAGAAACCAAAAGTCTACCGCTCGGAAGTCAACCAACAGGCG 660
    |||||
QY 201 Leuserseprovalthrlyserpheasnargglylucys 214
    |||||
    661 CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGT 702
    |||||
DB 661 CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGT 702
    |||||
RESULT 5
US-10-546-594-131
; Sequence 131, Application US/10546594
; Publication No. US20060086538A1
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: AOKI, Masahiko
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITAMI, Seima
; APPLICANT: UMEKI, Hiroe
```

```

? APPLICANT: SAIKAWA, Yoshitro
? APPLICANT: KUMAI, Koichiro
? APPLICANT: FUKUDA, Kazunasa
? TITLE OF INVENTION: MONOCLONAL ANTIBODY AND GENE ENCODING THE SAME, HYBRIDOMA, PHARM
? TITLE OF INVENTION: COMPOSITION, AND DIAGNOSTIC REAGENT
? FILE REFERENCE: 238067
? CURRENT APPLICATION NUMBER: US/10/546,594
? PRIOR FILING DATE: 2005-08-19
? PRIOR APPLICATION NUMBER: JP 2003/54670
? PRIOR FILING DATE: 2003-02-28
? PRIOR APPLICATION NUMBER: JP 2003/194643
? PRIOR FILING DATE: 2003-07-09
? NUMBER OF SEQ ID NOS: 132
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 131
? LENGTH: 705
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(705)
? OTHER INFORMATION:
? OS-10-546-594-131

```

Alignment Scores:	
Pred. No.:	7.74e-87
Score:	934.00
Percent Similarity:	92.5%
Best Local Similarity:	83.2%
Query Match:	83.7%
DB:	6
	0
	0
Length:	705
Matches:	177
Conservative:	20
Mismatches:	16
Indels:	1
Gaps:	0

US-10-635-908-15 (1-214) X US-10-546-594-131 (1-705)

QY	1	Asp1LevalMetThgInserGlnArgPheMetSerThrThxVal1LysAspValSer	20
Db	61	CACATCGTATATACCACGACTCTCCCTCCACCCTGTCTGCATCTGTAGAGACAAAGTCACC	120
QY	21	IlleThrCysValAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnIlyPro	40
Db	121	ATCATCTGGCCGGCCAGTCAGAGTATTAGTAGCTGGTGGCTCGTATCAGCAGAAACCA	180
QY	41	GlyInserProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp	60
Db	181	GGGAAAGCCCCCTTAAGCTCTCGATCTTAAGGCACTCAGTTTAAAGATGGGGGCCATCA	240
QY	61	ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer	80
Db	241	AGGTTTCAGGGGAGATGGATCTTGGAGACAAATTCATCTCCATCCAGCACCTCGCACT	300
QY	81	GluAspLeuValAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyIly	100
Db	301	GATGATTTTGGCAACTTATTACTGCCCAACAGTAAATAGTTATTCTPAACACTTTTGGCCAG	360
QY	101	GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro	120
Db	361	GGGACCAAGCTGGAGATCAACAGTCACCGTGGCGCAACATCTCTTCATCTTCCGCCCA	420
QY	121	SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr	140
Db	421	TCTGATGACAGTGAATCTGGAATCTGCACTGCTCTGTGTGTGCTCGTGAATTACTTAT	480
QY	141	ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln	160
Db	481	CCCAAGAGGCCCAAATTAACGTGGAAAGTGGATAACGCCCTTCCAATCGGTAATCTCCAG	540
QY	161	GlnSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr	180
Db	541	CAGAGTGTCAACAGACGACGACAGCAAGCAGACCACTACAGCTTCAGACACACCTTACG	600
QY	181	LeuSerLysValAspPyrGlnLysSerLysValTyrAlaCysGlnValThrHisGlnGly	200
Db	601	CTGAGCAAGACGACTACAGAAACCAAAAGTCTTACGCTCGCAAGTCAACCCATCAAGAGC	660

```

Oy      201  LeuserSerProValThrlYserPheAenA7G1Y1G1CYs  214
Db      661  CTGAGCTGCCCGCTACCAAGAAGCTTCAACAGGGAGAGTGT  702

RESULT 6
US-10-981-300-13
; Sequence 13, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABG4-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 642
; TYPE: DNA
; ORGANISM: homo sapien
US-10-981-300-13

```

Alignment Scores:	
Pred. No.:	8,71e-87
Score:	933.00
Percent Similarity:	92.1%
Best Local Similarity:	82.2%
Query Match:	83.6%
DB:	6
Length:	642
Matches:	176
Conservative:	21
Mismatches:	17
Indels:	0
Gaps:	0

US-10-635-908-15 (1-214) X US-10-981-300-13 (1-642)

```

OY 1 AsplIleValMeetThnGlnSerGlnArghPheMetSerThnValGlyAspArgValSer 20
Db 1 GACATCCGAGATGACCCAGCTTCCATCCCTCCCTGCTGCATCTGTAGGAACAGAGTCCAC 60
OY 21 IleThnGlySLySLaSerGlnAsnValValSerAlaValAlaTryptGlnGlnLysPro 40
Db 61 AGCATTTCCCGGCGCAGTCCAGACATTGACAAATTATTAGCTTGATATACGAGAAACCA 120
OY 41 GlyInserProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThnGlyValProAsp 60
Db 121 GGGAAAGTTCCTTAAGCTCTCTATCTATGCTGATCCATCCATTGGCAATCAGGGGCCATCT 180
OY 61 ArgPheThnGlySerGlySerGlyThraPheThnLeuThrIleSerAsnMetGlnSer 80
Db 181 CGTTTCAGTGGCAGTGGATCTTGCGACAGATTTCACCTCCACATCAGACGCTGCAGCCT 240
OY 81 GluAspLeuAlaAspPhePheCysGlnGlnIlyrSerAsnIlyrProThrPhrPheGlyGly 100
Db 241 GAAGATGTTGCACCTTATTACTGTCAAAAGTATACAGTCCGCCCGGAGCGTTGGCCCAA 300
OY 101 GlyThrIlyrSLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 301 GGGACCAAGGTGGAAATCAACAGCACTGGGCTGCACCATCTGTCTTCACTTTCCGGCCA 360
OY 121 SerAspGlnGlnLeuLysSerGlyThraLaserValValCysLeuLeuAsnAsnPheTyr 140
Db 361 TCTGATGAGCACTTGAATCTGGAACTGGCTCTGTTGTGTGCTGCTGTAATACTTCTAT 420
OY 141 ProArgGlnAlaLysValGlnIlyrPlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 421 CCCAAGAGGGCCCAAGATACAGTGAAGGTGAGATTAAGCCCTCCAAATCGGTAATCTCCAG 480
OY 161 GluSerValThnGlnGlnAspSerIlyAspSerThnTyrSerLeuSerSerThnLeuThr 180
Db 481 GAGAGTGTCCACGACGACAGACAGCAAGACACACACTTAACAGCTTCAGACGACCTTGACG 540
OY 181 LeuSerIlyValAspTyrGlnLysIlyrSLySLyValIlyrAlaCysGluValThnThsGlnGly 2000

```

D <sub>b</sub>	Q <sub>y</sub>	D <sub>b</sub>
541 CTGAGCAAGCAGACTACGAGAAACAAAGCTCAGCGCTGGAGAGTACCCATCAGGGC	201 LeuSerSerProValThrIySerPheAsnArgIyluCys	601 CTGAGCTCGCCCTCACAAAGAGCTCAACAGGGAGAGTGT
	214	642

## RESULT 7

```

US-11-155-444-3
; Sequence 3, Application US/11155444
; Publication No. US20060104971a1
; GENERAL INFORMATION:
; APPLICANT: GARBER, ELLEN
; APPLICANT: BAILLY, VERONIQUE
; APPLICANT: BROWNING, JEFFREY L.
; TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: BGNA168CN
; CURRENT APPLICATION NUMBER: US/11/155,444
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/US03/041393
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: 60/435,154
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/435,185
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: hucBE11/huBHA10 bispecific-1 antibody construct
; NAME/KEY: CDS
; LOCATION: (1)..(642)
; US-11-155-444-3

```

**Alignment Scores:**

Pred. No.:	2,22e-86	Length:	645
Score:	929.00	Matches:	176
Percent Similarity:	90.2%	Conservative:	17
Best Local Similarity:	82.2%	Mismatches:	21
Query Match:	83.2%	Indels:	0
DB:	7	Gaps:	0

US-10-635-908-15 (1-214) X US-11-155-444-3 (1-645)

[illegible][illegible]

## RESULT 8

```

US-11-211-917-47
; Sequence 47, Application US/11211917
; Publication No. US20060093600A1
; GENBANK INFORMATION:
; APPLICANT: BEDDIN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-47

```

Alignment Scores:

Pred. No.:	3.15e-86	length:	705
Score:	928.00	Matches:	177
Percent Similarity:	91.1%	Conservative:	18
Best Local Similarity:	82.7%	Mismatches:	19
Query Match:	83.2%	Indels:	0
DB:	7	Gaps:	0

US-10-635-908-15 (1-214) X US-11-211-917-47 (1-705)

QY 1 AsplIvalaMeTThGlnSerGlnArgPheMetSerThThValAlGlyAspAGValSer 20  
 Db 61 GACATCCAGATATACCCAGTCCATCTTCCTCCGTTCTGCATCTGTAGAGACAGATCACC 120  
 QY 21 ILeThrCybLysAlaSerGlnAsnValValSerAlaValAlaLTrpTyrGlnGlnLysPro 40  
 Db 121 ATCATCTGTGCGGCGCAGTCCAGGATATTTCACAGCTGGTATACCGGATATACGAAACCA 180  
 QY 41 GlyGlnSerProLysLeuLeuLeuLeuTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
 Db 181 GGGAAAGCCCCCTAACCTCTCGATCATATACTGCATTCACATTACAAAGTGGGGTCCCATCA 240  
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrLLeuSerAsnMetGlnSer 80  
 Db 241 AGCTTCAGGCGCAGTGTGATCTGGGACAGATTCATCTCACCATTCAGCAGCGCTGCAACCT 300  
 QY 81 GluAspLeuAlaAspPhePheCysGlnGlnLTrpSerAsnLTrpProTrpThrPheGlyGly 100

```
Db 301 GAAGTTTGGCACTTACTATTGTCACAGCGCTACATTTTCCTCCGCTCACTTCGCGCA 360
Qy 101 G1YThrlYsLeuGluIleYsAArgThrValAlaIalProSerValPheIlePheProPro 120
Db 361 GGGACCAAGGAGGAGATCAAGCAAGCACTGTGGCTGACCATCTGTCTTCACTTCCCGCA 420
Qy 121 SerAapGluGlnLeuIleYsSerGlyThrlAserValValCysLeuLeuAsnAsnPheTyr 140
Db 421 TCTGATGAGCAGATTGAAATCTGGAACTGCTCTGTGTGTGCTCTGCTAAATAACTTCAT 480
Qy 141 ProAagGluAlaIleYsValGlnTrpYsValAAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 481 CCCAGAGGCGCCAAAGTACAGAGGAGGAGGATTAAGCCCTTCATCCGGTAATCCCAAG 540
Qy 161 GluSerValThrlGluGlnAAspSerIlyAspSerThrlTyrSerLeuSerSerThrlLeuThr 180
Db 541 GAGAGTGTCAAGAGCAAGAGCAAGAGCAAGCACTACAGCCTCAGCAGCAGCAGCAGCAG 600
Qy 181 LeuSerIlyValAAspTyrGluIlyShiIlyYsValTyrAlaCysGluValThrlIleGlnIly 200
Db 601 CTGACCAAGCAGAGCTACAGAGAAACAAAGCTACGCTGGAAGTCAACCATCAGAGGC 660
Qy 201 LeuSerSerProValThrlYsSerPheAsnAArgIlyGluCys 214
Db 661 CTGAGCTGCGCCGTCAACAAAGAGCTTCAACAGGAGGAGAGTGT 702
```

## RESULT 9

```
US-11-211-917-87
; Sequence 87, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-87
```

## Alignment Scores:

```
Pred. No.: 1,76e-83 Length: 705
Score: 901.00 Matches: 173
Percent Similarity: 91.6% Conservative: 24
Best Local Similarity: 80.5% Mismatches: 16
Query Match: 80.7% Indels: 2
DB: 7 Gaps: 2
```

US-10-635-908-15 (1-214) x US-11-211-917-87 (1-705)

```
Qy 1 AapIleValMetThrlGlnSerGlnAryPheMetSerThrlValGlyAspAryValSer 20
Db 61 GAATTTGTGTGACGAGCTCCAGGACCTGTCTTGTCTCCAGGGGAGAAAGAGCCACC 120
Qy 21 IletHrCysLysAlaSerGlnAsnValValSerAla---ValAlaTrpTyrGlnGlnIly 39
Db 121 CTCCTCGAGGAGGAGGAGGAGGTGTACAGACCACTTACCTCGGTGTAACAGAGGAAA 180
Qy 40 ProGlyGlnSerProIlyLeuLeuIleTyrSerAlaSerAsnAArgTyrThrlGlyValPro 59
```

```
Db 181 CTGCGCAGGCTCCAGGCTCTCTCATATGCTGATCCAGACAGGCGCACTGGATCCCA 240
Qy 60 AapAryPheThrlGlySerGlySerGlyThrlAAspPheThrlLeuThrlIleSerAsnMetGln 79
Db 241 GACAGTTTCAGTGGAGAGGCTCTGGGACACATTCACCTTCACCATCAGACAGACTGGAG 300
Qy 80 SerGluAAspLeuAlaAAspPheCysGlnGlnIlyTyrSerAsnTyrProTyrThrlPheGly 99
Db 301 CCTGAAGATTTTGGAGTATATTACTGTACAGAGATTAATAGCTTA---TTCACTTCCGGC 357
Qy 100 GlyGlyThrlYsLeuGluIleYsAArgThrValAlaIalProSerValPheIlePhePro 119
Db 358 CCGGACCAAGATGAGATATCAAGAACTGTGGCTGACCATCTGTCTTCACTTCCCG 417
Qy 120 ProSerAapGluGlnLeuIleYsSerGlyThrlAserValValCysLeuLeuAsnAsnPhe 139
Db 418 CCATCTGATGAGCAGATTGAAATCTGGAACTGCTCTGTGTGTGCTCTGAAATAACTTC 477
Qy 140 TyrProAagGluAlaIleYsValGlnTrpYsValAAspAsnAlaLeuGlnSerGlyAsnSer 159
Db 478 TATCCAGAGGCGCCAAAGTACAGAGGAGGAGGATTAAGCCCTTCATCCGGTAATCC 537
Qy 160 GlnGluSerValThrlGluGlnAAspSerIlyAspSerThrlTyrSerLeuSerSerThrlLeu 179
Db 538 CAGAGAGTGTCAAGAGCAAGAGCAAGAGCAAGCACTACAGCCTCAGCAGCAGCAGCAG 597
Qy 180 ThrLeuSerIlyValAAspTyrGluIlyShiIlyYsValTyrAlaCysGluValThrlIleGln 199
Db 598 ACGCTGACCAAGCAGAGCTACAGAGAAACAAAGCTACGCTGGAAGTCAACCATCAG 657
Qy 200 GlyLeuSerSerProValThrlYsSerPheAsnAArgIlyGluCys 214
Db 658 GCGCTGAGCTGCCCTGTCACAAAGAGCTTCAACAGGAGGAGAGTGT 702
```

## RESULT 10

```
US-11-155-444-19
; Sequence 19, Application US/11155444
; Publication No. US20060104971A1
; GENERAL INFORMATION:
; APPLICANT: GARBER, EILEEN
; APPLICANT: BAILLY, VERONIQUE
; APPLICANT: BROWNING, JEFFREY L.
; TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
; FILE REFERENCE: BGNA168CN
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/US03/041393
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: 60/435,154
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/435,185
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 3.3
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CBB11 chimeric light
; OTHER INFORMATION: chain antibody construct
; NAME/KEY: CDS
; LOCATION: (1)..(642)
US-11-155-444-19
```

## Alignment Scores:

```
Pred. No.: 1,99e-83 Length: 645
Score: 900.00 Matches: 170
Percent Similarity: 89.3% Conservative: 21
Best Local Similarity: 79.4% Mismatches: 23
Query Match: 80.6% Indels: 0
```

DB: 7 Gaps: 0

US-10-635-908-15 (1-214) x US-11-155-444-19 (1-645)

QY 1 Aspl1eValMetThGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20  
 1 GATATTAAAGATGACCCAGTCTCCATCTTCATGTATGTCATGCGTGGAGAGAGAGTCACT 60

QY 21 IletThrCysAlaSerGlnAsnValValSerAlaValAlaTrpPyrGlnGlnLysPro 40  
 61 ATCACTGTAAGAGCGGCTCAGACATTAAAGCTATTAAAGCTGTAACAGAGAAACCA 120

QY 41 GlnGlnSerProLysLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60  
 121 TGGAAATCTCTTAAGATCTGTATCTATTTATGCAACAAAGTTGGCAGATGGGATCCCATCA 180

QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80  
 181 AGATTCAATGCGCATGCTGCGGCAAGATTATTTCTTAACCATCAAGCAGCCGTGAGTCT 240

QY 81 GluAspLeuAlaAspPheCysGlnGlnIleTyrSerAsnTyrProTrpThrPheGlyGly 100  
 241 GACGATACAGCAACTTATTATCTGTCTACAGCATGTCAGAGCCCGTGGAGCTTCGATGA 300

QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePhePro 120  
 301 GGCACCAAGCTGAGATCAAAACGACTGTGCTGCAACATCTGTCTTCACTTCCGCCCA 360

QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140  
 361 TCTGATGACGACAGTTGAATCTGGAACCTGCTGTGTGTGCTGCTGTAATTAATCTTCT 420

QY 141 ProArgGlnAlaLysValGlnTyrLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160  
 421 CCAGAGAGCCCAAGATGACGTGAAGGTGATTAACGCTCCAAATCGGCTAATCTCCAG 480

QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180  
 481 GAGAGTCTCAGACAGACAGACAGACAGACAGACAGACAGCCTCAGACAGACAGCCTGAGC 540

QY 181 LeuSerLysAlaAspTyrGlnLysValLysValTyrAlaCysGlnValThrIleGlnGly 200  
 541 CTGAGCAAGCAGACACTACGAGAAACCAAAAGTCTACGCTGCGAAGTCAACCCATCAGGGC 600

QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlnCys 214  
 601 CTGAGCTCGCCCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT 642

DB

RESULT 11  
 US-11-211-917-71  
 ; Sequence 71, Application US/11211917  
 ; Publication No. US2006093600A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BEDIAN, VAHE  
 ; APPLICANT: GLADUE, RONALD P.  
 ; APPLICANT: CORVALAN, JOSE  
 ; APPLICANT: JIA, XIAO-CHI  
 ; APPLICANT: FENG, XIAO  
 ; TITLE OF INVENTION: ANTIBODIES TO CD40  
 ; FILE REFERENCE: ABX-PF/3 US  
 ; CURRENT APPLICATION NUMBER: US/11/211,917  
 ; CURRENT FILING DATE: 2005-08-25  
 ; PRIOR APPLICATION NUMBER: US/10/292,088  
 ; PRIOR FILING DATE: 2002-11-08  
 ; PRIOR APPLICATION NUMBER: 60/348,980  
 ; NUMBER OF SEQ ID NOS: 147  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 71  
 ; LENGTH: 705  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-211-917-71

Alignment Scores:

Pred. No.: 3,846-81 Length: 705  
 Score: 878.00 Matches: 169  
 Percent Similarity: 90.7% Conservative: 26  
 Best Local Similarity: 78.6% Mismatches: 18  
 Query Match: 78.7% Indels: 2  
 DB: 7 Gaps: 2

US-10-635-908-15 (1-214) x US-11-211-917-71 (1-705)

QY 1 Aspl1eValMetThGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20  
 61 GAAATGTGTACGACAGTCTCCAGGACCTGTCTTGTCTCCAGGAGAAAGACCA 120

QY 21 IletThrCysAlaSerGlnAsnValValSerAlaValAlaTrpPyrGlnGlnLys 39  
 121 CTCTCTGACAGGCGCAGTCAAGTGTGACACAGAGCTTACCTGCGCAGCAGAAA 180

QY 40 ProGlnGlnSerProLysLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValPro 59  
 181 CTGGGCAAGGCTCCAGACTCTCTCATCTATGTGTCATCCAGAGGCGCACTGGCATCCA 240

QY 60 AspArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGln 79  
 241 GACAGGTTCAAGGACAGTGTGTCGAGACAGCTTCACTCTCACTCAGCAGACTGAG 300

QY 80 SerGlnAspLeuAlaAspPheCysGlnGlnIleTyrSerAsnTyrProTrpThrPheGly 99  
 301 CCGAAGATTTTGACGTGATTAATCTGACGACTGTGCGAAGCTTA---TTCACTTTCGCG 357

QY 100 GlyGlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePhePro 119  
 358 CCGGAGACCAAGTGATCAAAACGACTGTGCTGCAACATCTGTCTTCACTTCCCG 417

QY 120 ProSerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPhe 139  
 418 CCATCTGATGAGCAGTGTGAATCTGGAACCTGCTGTGTGTGCTGCTGTAATTAATCTTC 477

QY 140 TyrProArgGlnAlaLysValGlnTyrLysValAspAsnAlaLeuGlnSerGlyAsnSer 159  
 478 TATCCAGAGAGGCCAAAGTACAGTGAAGTGAATGAGCCCTCCATCGGGTAACTCC 537

QY 160 GlnGlnSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeu 179  
 538 CAGGAGAGTCTCAGACAGCAGACAGACAGACAGACAGCCTCAGCAGACAGCCTG 597

QY 180 ThrLeuSerLysAlaAspTyrGlnLysValLysValTyrAlaCysGlnValThrIleGln 199  
 598 ACCCTGAGCAAGCAGACTACGAGAAACCAAAAGTCTACGCTGCGAAGTCAACCCATCAG 657

QY 200 GlyLeuSerSerProValThrLysSerPheAsnArgGlyGlnCys 214  
 658 GGCCTGAGCTCGCCCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT 702

DB

RESULT 12  
 US-11-211-917-39  
 ; Sequence 39, Application US/11211917  
 ; Publication No. US2006093600A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BEDIAN, VAHE  
 ; APPLICANT: GLADUE, RONALD P.  
 ; APPLICANT: CORVALAN, JOSE  
 ; APPLICANT: JIA, XIAO-CHI  
 ; APPLICANT: FENG, XIAO  
 ; TITLE OF INVENTION: ANTIBODIES TO CD40  
 ; FILE REFERENCE: ABX-PF/3 US  
 ; CURRENT APPLICATION NUMBER: US/11/211,917  
 ; CURRENT FILING DATE: 2005-08-25  
 ; PRIOR APPLICATION NUMBER: US/10/292,088  
 ; PRIOR FILING DATE: 2002-11-08  
 ; PRIOR APPLICATION NUMBER: 60/348,980  
 ; PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 39  
LENGTH: 720  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-211-917-39

## Alignment Scores:

Pred. No.:	1,43e-80	Length:	720
Score:	872.50	Matches:	169
Percent Similarity:	86.8%	Conservative:	21
Best Local Similarity:	77.2%	Mismatches:	24
Query Match:	78.2%	Indels:	5
DB:	7	Gaps:	1

US-10-635-908-15 (1-214) x US-11-211-917-39 (1-720)

```
QY      1 AaplleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      61 GATATTGTGATATCACTCAAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGAGCGCGCTCC 120

QY      21 lIethrCyAlaValAspSerGlnAsnValVal-----SerAlaValAlaTTP 35
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      121 ATCTCTGCAAGCTCTAGTCAAGAGTCTTCTGTATAGTATGATGATACAACTATTGATTGG 180

QY      36 TrrGlnGlnLysProGlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTy 55
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      181 TACCTGCAAGAGCCAGGAGGAGTCTCCACAGCTCTGATCATTTGGGTTCTAATCGGGCC 240

QY      56 ThrGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuTrile 75
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      241 TCCGGGGTCCCTGACAGGTTCACTGAGTCAAGTCAAGATTTTACACTGAAATTC 300

QY      76 SerAsnMetGlnSerGlnAspLeuAlaAspPhePheCyGlnGlnIntySerAsnTyPro 95
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      301 AGCAGAGTGAAGGCTAGATGTTGGGGTTATTACTGATGATGAAGTTTACAAACTCCA 360

QY      96 TrrThrPheGlyGlyGlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerVal 115
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      361 TTCACCTTCCGGCCCTGGAGCAAAAGTGATATCAAAAGAACTGTGCTGCACCATCTGTC 420

QY      116 PheIlePheProProSerAspGlnGlnLeuLysSerGlyThrAlaSerValValCyBlau 135
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      421 TTCATCTTCCCGCATCTGATGAGAGGTTGAATCTGAAATCTGAACTGCTGTGTGTGCTCG 480

QY      136 LeuAsnAsnPheTyProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGln 155
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      481 CTGAATTAACCTTCTATCCCAAGAGGCCAAAGTACAGTGAAGGTGAATACCGCTCCCA 540

QY      156 SerGlyAsnSerGlnGlnSerValThrGlnAspSerLysAspSerThrTySerLeu 175
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      541 TCGGTAACCTCCAGAGAGAGTGTCAAGAGCAGAGACGCAAGCACTACACCTC 600

QY      176 SerSerThrLeuThrLeuSerLysAlaAspTyGlnLysIleLysValTyraIaCyBgln 195
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      601 AGCAGACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTTACGCTCGGAA 660

QY      196 ValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGlyCy 214
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      661 GTCAACCATCAAGGCTGAGCTCGCCCTGTCACAAAGAGCTTCAACAGGGAGAGTGT 717
```

## RESULT 13

US-11-211-917-31  
Sequence 31, Application US/11211917  
Publication No. US20060093600A1  
GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: PENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CP40

FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/11/211,917  
CURRENT FILING DATE: 2005-08-25  
PRIOR APPLICATION NUMBER: US/10/292,088  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 720  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-211-917-31

## Alignment Scores:

Pred. No.:	2,88e-80	Length:	720
Score:	869.50	Matches:	169
Percent Similarity:	86.3%	Conservative:	20
Best Local Similarity:	77.2%	Mismatches:	25
Query Match:	77.9%	Indels:	5
DB:	7	Gaps:	1

US-10-635-908-15 (1-214) x US-11-211-917-31 (1-720)

```
QY      1 AaplleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      61 GATATTGTGATATCACTCAAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGAGCGCGCTCC 120

QY      21 lIethrCyAlaValAspSerGlnAsnValVal-----SerAlaValAlaTTP 35
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      121 ATCTCTGCAAGCTCTAGTCAAGAGCTCTCCACTCACTAATGATGATACAACTATTGATTGG 180

QY      36 TrrGlnGlnLysProGlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTy 55
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      181 TACCTGCAAGAGCCAGGAGGAGTCTCCACAACTCTGATCATTTGGGTTCTAATCGGGCC 240

QY      56 ThrGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuTrile 75
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      241 TCCGGGGTCCCTGACAGGTTCACTGAGTCAAGTCAAGATTTTACACTGAAATTC 300

QY      76 SerAsnMetGlnSerGlnAspLeuAlaAspPhePheCyGlnGlnIntySerAsnTyPro 95
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      301 AGCAGAGTGAAGGCTAGATGTTGGGGTTATTACTGATGATGAAGTTTACAAACTCCG 360

QY      96 TrrThrPheGlyGlyGlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerVal 115
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      361 TACAGTTTGGCCAGGAGGAGCAAGCTGAGATCAAAAGAACTGTGCTGCACCATCTGTC 420

QY      116 PheIlePheProProSerAspGlnGlnLeuLysSerGlyThrAlaSerValValCyBlau 135
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      421 TTCATCTTCCCGCATCTGATGAGAGGTTGAATCTGAAATCTGAACTGCTGTGTGTGCTCG 480

QY      136 LeuAsnAsnPheTyProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGln 155
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      481 CTGAATTAACCTTCTATCCCAAGAGGCCAAAGTACAGTGAAGGTGAATACCGCTCCCA 540

QY      156 SerGlyAsnSerGlnGlnSerValThrGlnAspSerLysAspSerThrTySerLeu 175
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      541 TCGGTAACCTCCAGAGAGAGTGTCAAGAGCAGAGACGCAAGCACTACACCTC 600

QY      176 SerSerThrLeuThrLeuSerLysAlaAspTyGlnLysIleLysValTyraIaCyBgln 195
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      601 AGCAGACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTTACGCTCGGAA 660

QY      196 ValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGlyCy 214
        |||.....|.....|.....|.....|.....|.....|.....|.....|
DB      661 GTCAACCATCAAGGCTGAGCTCGCCCTGTCACAAAGAGCTTCAACAGGGAGAGTGT 717
```

## RESULT 14

US-11-293-697-1838  
Sequence 1838, Application US/11293697  
Publication No. US20060105376A1



```
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: H1-A0106
/ CURRENT APPLICATION NUMBER: US/11/293,697
/ CURRENT FILING DATE: 2005-12-05
/ PRIOR APPLICATION NUMBER: US/10/108,260
/ PRIOR FILING DATE: 2002-03-28
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1838
/ LENGTH: 929
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-293-697-1838

Alignment Scores:
Pred. No.: 5,61e-80 Length: 929
Score: 868.00 Matches: 166
Percent Similarity: 86.9% Conservative: 20
Best Local Similarity: 77.6% Mismatches: 28
Query Match: 77.8% Indels: 0
DB: Gaps: 0

US-10-635-908-15 (1-214) x US-11-293-697-1838 (1-929)

QY 1 AsplleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB 91 GACACTCAGATGAGCCAGCTCCGACCTCCCTGTCGATCTGGAGGACAGAGTCACC 150
QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTrpTyrglnGlnLysPro 40
DB 151 ATACCTTCCAGCGAGCGATCAGCATGTAAATTTTAAACGGTATCGTCAACCA 210
QY 41 GlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
DB 211 GGCAGAGCCCTAAGCCCTCATCCACGATGCGCTCCAGTACAGAAAAGAGTCCCA 270
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 271 AGATTCAAGTGAAGTGAATTGGACAGATTGTTTTCATCAACCAACCTACCAACT 330
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIleTySerAsnTyProTrpThrPheGly 100
DB 331 GAAGATGTCGACATATTACTGTCAACAATTGCTCTCTGCTCGGACCTTTGGCAG 390
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePhePro 120
DB 391 GGGACCAAGCTTCAGATCAATCGAACTGGCTGCACCATCTCTTCATCTTCCGCCA 450
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPhe 140
DB 451 TCTGATAGCAGGTTGAATCTGGAATGCTCTGTGTGTGCTGCTGAATTAACCTTCT 510
QY 141 ProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 511 CCCGAGAGGCCAAGTACAGTGAAGTGAATTAACCCCTCCATAGGGTAACTCCAG 570
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 180
DB 571 GAGAGTGTCAAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 630
QY 181 LeuSerLysAlaAspTyThrGlnLysLysValTyThrAlaCysGlnValThrHisGln 200
DB 631 CTGAGCAAGCAGCTACGAGAAACACAAAGTCTACGCTGCGAGTCAACCAACGAG 690
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlnCys 214
DB 691 CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 732

RESULT 15
US-11-211-917-15
/ Sequence 15, Application US/11211917
```

```
/ Publication No. US20060093600A1
/ GENERAL INFORMATION:
/ APPLICANT: BEDIAN, VARE
/ APPLICANT: GLADUE, RONALD P.
/ APPLICANT: CORVALAN, JOSE
/ APPLICANT: JIA, XIAO-CHI
/ APPLICANT: FENG, XIAO
/ TITLE OF INVENTION: ANTIBODIES TO CD40
/ FILE REFERENCE: ABX-PF/3 US
/ CURRENT APPLICATION NUMBER: US/11/211,917
/ CURRENT FILING DATE: 2005-08-25
/ PRIOR APPLICATION NUMBER: US/10/292,088
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: 60/348,980
/ PRIOR FILING DATE: 2001-11-09
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 15
/ LENGTH: 720
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-211-917-15

Alignment Scores:
Pred. No.: 4,6e-80 Length: 720
Score: 867.50 Matches: 169
Percent Similarity: 86.3% Conservative: 20
Best Local Similarity: 77.2% Mismatches: 25
Query Match: 77.7% Indels: 5
DB: Gaps: 1

US-10-635-908-15 (1-214) x US-11-211-917-15 (1-720)

QY 1 AsplleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB 61 GATATTGTGATGATCTAGTCTCCACTCCCTCCGCTACCCCTGAGAGCCGGCTCC 120
QY 21 IleThrCysLysAlaSerGlnAsnValVal-----SerAlaValAlaTrp 35
DB 121 ATCTCTGACAGCTAGTATGACAGCTCTTGTATAGTATGATGATACAACTTTTGATTGG 180
QY 36 TyrGlnGlnLysProGlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTy 55
DB 181 TACCTCAGAGAGCAGGAGGAGCTCCACACCTCTGATCTAATTTGGCTTCAATCGGCC 240
QY 56 ThrGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuThr 75
DB 241 TCCGGGGTCCCTTACAGGTTCACTGAGCAGTGAATTTTACCTGAAATC 300
QY 76 SerAsnMetGlnSerGlnAspLeuAlaAspPheCysGlnGlnIleTySerAsnTyPro 95
DB 301 AGCAGAGTGAAGGCTGAGATGTTGGGGTTATTATTCATGACAGCTTCAAACTCCT 360
QY 96 TrpThrPheGlyGlyGlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerVal 115
DB 361 CGGACGTTCCGCAAGGAGCAAGTGAATCAAGAACTGTGGCTGCACATCTGTC 420
QY 116 PheIlePheProProSerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeu 135
DB 421 TTCACTTCCCGCATGTGATGACAGCTTGAATCTGGAATCTGCTGTGTGTGCTG 480
QY 136 LeuAsnAsnPheTyProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGln 155
DB 481 CTGAATAACTTCTATCCCAAGAGGCCAAAGTACAGTGAAGTGAATACGCCCTCCA 540
QY 156 SerGlyAsnSerGlnGlnSerValThrGlnGlnAspSerLysAspSerThrTySerLeu 175
DB 541 TCGGTAACTCCCAAGGAGAGTGCACAGACAGGACGAAAGCAGACACCTTACAGCTC 600
QY 176 SerSerThrLeuThrLeuSerLysAlaAspTyThrGlnLysLysValTyThrAlaCysGln 195
DB 601 AGCAGACCTCTGACGCTGAGCAAGCAGACGACTGAGAAAACAAAGTCTACGCTGCGAA 660
```

Oy 196 ValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214  
 |||||  
 Db 661 GTCACCCATCAGGGCCTGAGCTGCGCCGTCAACAAGAGCTCAACAGGGAGAGTGT 717  
 |||||

Search completed: June 3, 2006, 09:17:10  
 Job time : 28.4204 secs